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From: Kaufman, Claire  
Sent: Tuesday, November 23, 2004 11:52 AM  
To: STIC-Biotech/ChemLib  
Subject: sequence 09/783,931

SEQUENCE SEARCH REQUEST

Examiner: Claire Kaufman AU: 1646 MAILBOX: Rem 4C70  
Room: Rem 4E85 Serial #: 09/783,931 Date: 12/23/04

Please search SEQ ID NO: 2, 12, 13, 23 in commercial and interference databases.

Thanks,  
Claire Kaufman, AU 1646  
Rem 4E85 (571) 272-0873

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\*\*\*\*\*

STAFF USE ONLY

Searcher: \_\_\_\_\_  
Searcher Phone: 2-\_\_\_\_\_  
Date Searcher Picked up: \_\_\_\_\_  
Date Completed: \_\_\_\_\_  
Searcher Prep/Rev. Time: \_\_\_\_\_  
Online Time: \_\_\_\_\_

\*\*\*\*\*

Type of Search

NA Sequence: # \_\_\_\_\_  
AA Sequence: # \_\_\_\_\_  
Structure: # \_\_\_\_\_  
Bibliographic: \_\_\_\_\_  
Litigation: \_\_\_\_\_  
Patent Family: \_\_\_\_\_  
Other: \_\_\_\_\_

\*\*\*\*\*

Vendors and cost where applicable

STN: \_\_\_\_\_  
DIALOG: \_\_\_\_\_  
QUESTEL/ORBIT: \_\_\_\_\_  
LEXIS/NEXIS: \_\_\_\_\_  
SEQUENCE SYSTEM: \_\_\_\_\_  
WWW/Internet: \_\_\_\_\_  
Other(Specify): \_\_\_\_\_

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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

# OM protein - protein search, using sw model

Run on: December 2, 2004, 03:52:57 ; Search time 40 Seconds  
(without alignments)  
290.141 Million cell updates/sec

Title: US-09-783-931-23

Perfect score: 926

Sequence: 1 TNNLANCQREKDISVSIIG.....DTKYSVVYSEKDECVIA 175

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

## Database :

Issued Patents AA:\*  
1: /cgn2\_6/prodata/1/iaa/5A COMB pep:\*  
2: /cgn2\_6/prodata/1/iaa/5B COMB pep:\*  
3: /cgn2\_6/prodata/1/iaa/6A COMB pep:\*  
4: /cgn2\_6/prodata/1/iaa/6B COMB pep:\*  
5: /cgn2\_6/prodata/1/iaa/6C COMB pep:\*  
6: /cgn2\_6/prodata/1/iaa/backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	916	98.9	175	3	US-08-981-392-23
2	916	98.9	175	4	US-09-908-322-23
3	631.5	68.2	118	3	US-08-981-392-17
4	631.5	68.2	118	4	US-09-908-322-17
5	527.5	57.0	702	3	US-09-068-740A-4
6	527.5	57.0	723	3	US-09-068-740A-9
7	527.5	57.0	723	4	US-09-423-753-27
8	527.5	57.0	723	4	US-09-641-612-6
9	527.5	57.0	723	3	US-10-140-002-346
10	448	48.4	713	3	US-08-872-855-5
11	428	46.2	720	3	US-08-872-855-4
12	419	45.2	722	3	US-08-981-392-12
13	419	45.2	722	4	US-09-908-322-12
14	388	41.9	728	3	US-08-981-392-2
15	388	41.9	728	4	US-09-908-322-2
16	388	41.9	729	3	US-08-872-855-8
17	359.5	38.8	187	3	US-08-981-392-46
18	359.5	38.8	187	4	US-09-908-322-46
19	356	38.4	721	3	US-08-872-855-7
20	356	38.4	721	3	US-08-981-392-5
21	356	38.4	721	4	US-09-908-322-5
22	294.5	31.8	717	3	US-08-872-855-9
23	197	21.3	578	3	US-08-981-392-13
24	197	21.3	578	4	US-09-908-322-13
25	167	18.0	173	3	US-08-981-392-18
26	167	18.0	173	4	US-09-908-322-18
27	127.5	13.8	685	3	US-08-872-855-2

28 127.5 13.8 685 4 US-09-641-612-7 Sequence 7, Appli  
29 126.5 13.7 659 4 US-09-423-753-3 Sequence 1, Appli  
30 126.5 13.7 685 4 US-09-423-753-25 Sequence 25, Appli  
31 126.5 13.7 685 4 US-10-140-002-88 Sequence 88, Appli  
32 125 13.5 26 3 US-08-981-392-77 Sequence 77, Appli  
33 125 13.5 26 4 US-09-908-322-77 Sequence 77, Appli  
34 88.5 9.6 1106 4 US-09-538-092-874 Sequence 874, Appli  
35 82 8.9 407 4 US-09-468-433C-26 Sequence 26, Appli  
36 81 8.7 233 4 US-09-311-021-46 Sequence 46, Appli  
37 81 8.7 330 4 US-09-252-991A-24637 Sequence 24637, A  
38 80.5 8.7 950 4 US-10-009-332-1 Sequence 1, Appli  
39 77 8.3 127 4 US-09-489-039A-8856 Sequence 8856, Ap  
40 76.5 8.3 874 3 US-09-369-364A-15 Sequence 15, Appli  
41 75 8.1 439 4 US-09-724-797-86 Sequence 86, Appli  
42 75 8.1 3025 6 5223423-3 Patent No. 5223423  
43 74.5 8.0 78 4 US-09-252-991A-19604 Sequence 19604, A  
44 74.5 8.0 129 4 US-09-252-991A-16731 Sequence 16731, A  
45 74.5 8.0 157 4 US-09-252-991A-31989 Sequence 31989, A

## ALIGNMENTS

## RESULT 1

US-08-981-392-23  
; Sequence 23, Application US/08981392  
; Patent No. 6262025  
; GENERAL INFORMATION:  
; APPLICANT: Igh-Horowicz, David  
; APPLICANT: Henrique, Domingos Manuel Pinto  
; APPLICANT: Lewis, Julian Hart  
; APPLICANT: Atavanis-Teakonas, Spyridon  
; APPLICANT: Gray, Grace  
; TITLE OF INVENTION: NUCLEOTIDE AND PROTEIN SEQUENCES  
; TITLE OF INVENTION: OF VERTEBRATE DELTA GENES AND METHODS BASED THEREON  
; NUMBER OF SEQUENCES: 94  
; CORRESPONDENCE ADDRESS:  
; ADDRESSER: Pennie & Edmonds LLP  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: NY  
; COUNTRY: USA  
; ZIP: 10036/2711  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/981,392  
; FILING DATE: 22-DEC-1997  
; CLASSIFICATION: 514  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Antler, Adriane M.  
; REGISTRATION NUMBER: 32,605  
; REFERENCE/DOCKET NUMBER: 7326-038  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 212-790-9090  
; TELEFAX: 212-869-8864  
; INFORMATION FOR SEQ ID NO: 23:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 175 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: unknown  
; MOLECULE TYPE: peptide  
US-08-981-392-23

Query Match 98.9%; Score 916; DB 3; Length 175;  
Best Local Similarity 100.0%; Pred. No. 6.3e-97;  
Matches 175; Conservative 0; Mismatches 0; Indels 0; Gaps 0;



Lewis, Julian Hart  
Artavanis-Taskonas, Spyridon  
Gray, Grace  
TITLE OF INVENTION: NUCLEOTIDE AND PROTEIN SEQUENCES OF  
VERTEBRATE DELTA GENE AND METHODS BASED THEREON  
NUMBER OF SEQUENCES: 94  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pennie & Edmonds LLP  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: NY  
COUNTRY: USA  
ZIP: 10036/2711  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/908,322  
FILING DATE: 17-Jul-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/981,392  
FILING DATE: 22-DEC-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Mirock, S Leslie  
REGISTRATION NUMBER: 18,872  
REFERENCE/DOCKET NUMBER: 7326-123  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 212-790-9090  
TELEFAX: 212-869-8864  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 17:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 118 amino acids  
TYPE: amino acid  
STRANDEDNESS: <Unknown>  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
SEQUENCE DESCRIPTION: SEQ ID NO: 17:  
US-09-908-322-17  
Query Match 68.2%; Score 631.5; DB 4; Length 118;  
Best Local Similarity 99.2%; Pred. No. 1.4e-64;  
Matches 118; Conservative 0; Mismatches 0; Indels 1; Gaps 1;  
QY 57 LVQDLKGGDDTAVRTSHSKRDTKCQSPGSSRRRGPRPHSGXACCGPGSGGGTGWYSSWNH 116  
Db 1 LVQDLKGGDDTAVRTSHSKRDTKCQSPGSSRRRGPRPHSGXACCGPGSGGGTGWYSSW-H 59  
QY 117 CSVSLPKCSHAFIVDFLYFPFSGEASERKRPDSGCGSTSKDTKYQSVYVISEBKDECVIA 175  
Db 60 CSVSLPKCSHAFIVDFLYFPFSGEASERKRPDSGCGSTSKDTKYQSVYVISEBKDECVIA 118  
RESULT 5  
US-09-068-740A-4  
; Sequence 4, Application US/09068740A  
; Patent No. 6337387  
; GENERAL INFORMATION:  
; APPLICANT: SAKANO, SEIJI  
; APPLICANT: ITOH, AKIRA  
; TITLE OF INVENTION: DIFFERENTIATION-SUPPRESSIVE POLYPEPTIDE  
; FILE REFERENCE: KP-8447  
; CURRENT APPLICATION NUMBER: US/09/068,740A  
; CURRENT FILING DATE: 1998-06-18  
; PRIOR APPLICATION NUMBER: JP 7-299611  
; PRIOR FILING DATE: 1995-11-17  
; PRIOR APPLICATION NUMBER: JP 7-311811  
; PRIOR FILING DATE: 1995-11-30  
; PRIOR APPLICATION NUMBER: PCT/JP96/03356  
; PRIOR FILING DATE: 1996-11-15  
; SOFTWARE: Patent In Ver. 2.1  
; NUMBER OF SEQ ID NOS: 48  
; SEQ ID NO 9  
; LENGTH: 723  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-068-740A-9  
Query Match 57.0%; Score 527.5; DB 3; Length 723;  
Best Local Similarity 64.8%; Pred. No. 1.3e-51;  
Matches 114; Conservative 4; Mismatches 13; Indels 45; Gaps 4;  
QY 1 TNNLANCQREKDISVSIIGATGIXNTNKKADFXDXGSSDKNQKARYPSVDYNLVQD 60  
Db 589 TNNLANCQREKDISVSIIGATGIXNTNKKADFXDXGSSDKNQKARYPSVDYNLVQD 646  
QY 61 LKGGDDTAVRTSHSKRDTKCQSPGSSRRRG-PRPHSGXACCGPGSGGGTGWYSSWNHCSV 119  
Db 647 LKGGDDTAVRTSHSKRDTKCQSPGSSRRRG-PRPHSGXACCGPGSGGGTGWYSSWNHCSV 683  
QY 120 SLPKCSHAFIVDFLYFPFSGEASERKRPDSGCGSTSKDTKYQSVYVISEBKDECVIA 175  
Db 684 -----GEASERKRPDSGCGSTSKDTKYQSVYVISEBKDECVIA 720  
RESULT 7  
US-09-423-753-27  
; Sequence 27, Application US/09423753  
; Patent No. 6664098  
; GENERAL INFORMATION:  
; APPLICANT: SAKANO, SEIJI

NUMBER OF SEQ ID NOS: 48  
; SOFTWARE: Patent In Ver. 2.1  
; SEQ ID NO 4  
; LENGTH: 702  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-068-740A-4  
Query Match 57.0%; Score 527.5; DB 3; Length 702;  
Best Local Similarity 64.8%; Pred. No. 1.2e-51;  
Matches 114; Conservative 4; Mismatches 13; Indels 45; Gaps 4;  
QY 1 TNNLANCQREKDISVSIIGATGIXNTNKKADFXDXGSSDKNQKARYPSVDYNLVQD 60  
Db 568 TNNLANCQREKDISVSIIGATGIXNTNKKADFXDXGSSDKNQKARYPSVDYNLVQD 625  
QY 61 LKGGDDTAVRTSHSKRDTKCQSPGSSRRRG-PRPHSGXACCGPGSGGGTGWYSSWNHCSV 119  
Db 626 LKGGDDTAVRTSHSKRDTKCQSPGSSRRRG-PRPHSGXACCGPGSGGGTGWYSSWNHCSV 662  
QY 120 SLPKCSHAFIVDFLYFPFSGEASERKRPDSGCGSTSKDTKYQSVYVISEBKDECVIA 175  
Db 663 -----GEASERKRPDSGCGSTSKDTKYQSVYVISEBKDECVIA 699  
RESULT 6  
US-09-068-740A-9  
; Sequence 9, Application US/09068740A  
; Patent No. 6337387  
; GENERAL INFORMATION:  
; APPLICANT: SAKANO, SEIJI  
; APPLICANT: ITOH, AKIRA  
; TITLE OF INVENTION: DIFFERENTIATION-SUPPRESSIVE POLYPEPTIDE  
; FILE REFERENCE: KP-8447  
; CURRENT APPLICATION NUMBER: US/09/068,740A  
; CURRENT FILING DATE: 1998-06-18  
; PRIOR APPLICATION NUMBER: JP 7-299611  
; PRIOR FILING DATE: 1995-11-17  
; PRIOR APPLICATION NUMBER: JP 7-311811  
; PRIOR FILING DATE: 1995-11-30  
; PRIOR APPLICATION NUMBER: PCT/JP96/03356  
; PRIOR FILING DATE: 1996-11-15  
; NUMBER OF SEQ ID NOS: 48  
; SOFTWARE: Patent In Ver. 2.1  
; SEQ ID NO 9  
; LENGTH: 723  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-068-740A-9  
Query Match 57.0%; Score 527.5; DB 3; Length 723;  
Best Local Similarity 64.8%; Pred. No. 1.3e-51;  
Matches 114; Conservative 4; Mismatches 13; Indels 45; Gaps 4;  
QY 1 TNNLANCQREKDISVSIIGATGIXNTNKKADFXDXGSSDKNQKARYPSVDYNLVQD 60  
Db 589 TNNLANCQREKDISVSIIGATGIXNTNKKADFXDXGSSDKNQKARYPSVDYNLVQD 646  
QY 61 LKGGDDTAVRTSHSKRDTKCQSPGSSRRRG-PRPHSGXACCGPGSGGGTGWYSSWNHCSV 119  
Db 647 LKGGDDTAVRTSHSKRDTKCQSPGSSRRRG-PRPHSGXACCGPGSGGGTGWYSSWNHCSV 683  
QY 120 SLPKCSHAFIVDFLYFPFSGEASERKRPDSGCGSTSKDTKYQSVYVISEBKDECVIA 175  
Db 684 -----GEASERKRPDSGCGSTSKDTKYQSVYVISEBKDECVIA 720  
RESULT 7  
US-09-423-753-27  
; Sequence 27, Application US/09423753  
; Patent No. 6664098  
; GENERAL INFORMATION:  
; APPLICANT: SAKANO, SEIJI



```
;
; ATTORNEY/AGENT INFORMATION:
; NAME: Arnold, Beth E.
; REGISTRATION NUMBER: 35,430
; REFERENCE/DOCKET NUMBER: MAA-003.02
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-832-1000
; TELEFAX: 617-832-7000
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 713 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
;
US-08-872-855-5
Query Match 48.4%; Score 448; DB 3; Length 713;
Best Local Similarity 54.3%; Pred. No. 1.6e-42;
Matches 95; Conservative 13; Mismatches 23; Indels 44; Gaps 3;

QY 1 TNNLANCOREKDISVSIIGATGIXNTNKKADPFXGDXSDKNGFQKARYPSVDYNLVOD 60
Db 580 TNNLANCOREKDVSVSIIGATQIKNTNKKADP-HGDHGAKKSSF-KARYPTVDYNLIRD 637
QY 61 LKGDDTAVRTSHSKRDTKQSPGSGRRRPRPHSGXACCGPGSGGTGWSVSSNNHCSVS 120
Db 638 LKGDENVADAKSKRDTKQSGSAGEEKSTLTGR----- 673
QY 121 LPKCSHAFTVDFLYPFPFSGEASERKRPDSCGTSKDTKYQSVYVISEEKDECVIA 175
Db 674 -----GEVPRKRPESVYSTSKDTKYQSVYVLSAEKDECVIA 710

RESULT 11
US-08-872-855-4
; Sequence 4, Application US/08872855
; Patent No. 6121045
; GENERAL INFORMATION:
; APPLICANT: McCarthy, Sean
; APPLICANT: Gearing, David
; TITLE OF INVENTION: NOVEL HUMAN DELTA3 COMPOSITIONS AND
; TITLE OF INVENTION: THERAPEUTIC USES THEREFOR
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: POLSKY, HOAG & ELIOT LLP
; STREET: One Post Office Square
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109-2170
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/872,855
; FILING DATE: 11-JUN-1997
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Arnold, Beth E.
; REGISTRATION NUMBER: 35,430
; REFERENCE/DOCKET NUMBER: MAA-003.02
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-832-1000
; TELEFAX: 617-832-7000
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 720 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
;

US-08-872-855-4
Query Match 46.2%; Score 428; DB 3; Length 720;
Best Local Similarity 53.7%; Pred. No. 3.1e-40;
Matches 94; Conservative 12; Mismatches 25; Indels 44; Gaps 4;

QY 1 TNNLANCOREKDISVSIIGATGIXNTNKKADPFXGDXSDKNGFQKARYPSVDYNLVOD 60
Db 587 TNNLANCOREKDVSVSIIGATQIKNTNKKADP-HGDHGAKKSSF-KVRYPTVDYNLVRD 644
QY 61 LKGDDTAVRTSHSKRDTKQSPGSGRRRPRPHSGXACCGPGSGGTGWSVSSNNHCSVS 120
Db 645 LKGDENVADTSHSKRDTKQSGSAGEEK-----IAPTLRG----- 680
QY 121 LPKCSHAFTVDFLYPFPFSGEASERKRPDSCGTSKDTKYQSVYVISEEKDECVIA 175
Db 681 -----GEIPDRKRPESVYSTSKDTKYQSVYVLSAEKDECVIA 717

RESULT 12
US-08-981-392-12
; Sequence 12, Application US/08981392
; Patent No. 6262025
; GENERAL INFORMATION:
; APPLICANT: Ish-Horowicz, David
; APPLICANT: Henrique, Domingos Manuel Pinto
; APPLICANT: Lewis, Julian Hart
; APPLICANT: Artavanis-Teakonas, Spyridon
; APPLICANT: Gray, Grace
; TITLE OF INVENTION: NUCLEOTIDE AND PROTEIN SEQUENCES
; TITLE OF INVENTION: OF VERTEBRATE DELTA GENES AND METHODS BASED THEREON
; NUMBER OF SEQUENCES: 94
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036/2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/981,392
; FILING DATE: 22-DEC-1997
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Atler, Adriane M.
; REGISTRATION NUMBER: 32,605
; REFERENCE/DOCKET NUMBER: 7326-038
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-790-9090
; TELEFAX: 212-869-8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 722 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
;
US-08-981-392-12
Query Match 45.2%; Score 419; DB 3; Length 722;
Best Local Similarity 52.6%; Pred. No. 3.3e-39;
Matches 92; Conservative 12; Mismatches 27; Indels 44; Gaps 4;

QY 1 TNNLANCOREKDISVSIIGATGIXNTNKKADPFXGDXSDKNGFQKARYPSVDYNLVOD 60
Db 589 TNNLANCOREKDVSVSIIGATQIKNTNKKADP-HGDHGAKKSSF-KVRYPTVDYNLVRD 646
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Lewis, Julian Hart
Artavanis-Tsakonas, Spyridon
Gray, Grace
TITLE OF INVENTION: NUCLEOTIDE AND PROTEIN SEQUENCES OF
VERTEBRATE DELTA GENE AND METHODS BASED THEREON
NUMBER OF SEQUENCES: 94
CORRESPONDENCE ADDRESS:
ADDRESSER: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10036/2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/908,322
FILING DATE: 17-Jul-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/981,392
FILING DATE: 22-DEC-1997
ATTORNEY/AGENT INFORMATION:
NAME: Mirarock, S Leelie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 7326-123
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-790-9090
TELEFAX: 212-869-8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 728 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: unknown
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-908-322-2

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Query Match 41.9%; Score 388; DB 4; Length 728;
Best Local Similarity 49.7%; Pred.No. 1.2e-35;
Matches 87; Conservative 15; Mismatches 27; Indels 46; Gaps 5;

QY 1 TMNNLANCOREKDISVIGATGIXNTNKKADFXGDXSSDKNGFKARYPVDYNLVQD 60
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
597 TMNNLANCOREKDISVIGATGIXNTNKKADFXGDXSSDKNGFKARYPVDYNLVHE 653
QY 61 LKGDPTAVTSHSKDTHKQSPGSGRRRGRPHSGXACCPCGGGTGWSVWNCVS 120
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
654 LKNEP-SVKEHGKCEAKETDSEAEKS-----AVQ 685
QY 121 LPKCSHAFIVDFLYPFPSGEASERKRPDSGCSTSKDTKYQSVVIVSEKDECVIA 175
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
686 LK-----SSTSERKRPDSVYSTSKDTKYQSVVIVSEKDECVIA 725

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Search completed: December 2, 2004, 04:03:16  
Job time : 66 secs

**This Page Blank (uspto)**

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 2, 2004, 03:52:12 ; Search time 194 Seconds  
(without alignments)  
519.024 Million cell updates/sec

Title: US-09-783-931-23  
Perfect score: 926  
Sequence: 1 TNNLANCOREKDISVSIIG.....DTKYQSVYVISEKDECVIA 175

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

Database : UniProt\_02: \*  
1: uniprot\_sprot: \*  
2: uniprot\_trembl: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	527.5	57.0	723	1 DL11_HUMAN	O00548 homo sapien
2	445	48.1	714	1 DL11_RAT	P97677 rattus norv
3	431	46.5	722	2 Q6P5V7	Q6P5V7 mus musculu
4	431	46.5	722	2 AAH57400	AAH57400 mus muscu
5	431	46.5	722	2 AAR30869	AAR30869 mus muscu
6	431	46.5	722	2 AAH65063	AAH65063 mus muscu
7	428	46.2	722	1 DL11_MOUSE	Q06556 gallus gall
8	388	41.9	728	2 Q90656	Q90656 gallus gall
9	387.5	41.8	726	2 Q8AM87	Q8AM87 xenopus lae
10	356	38.4	721	2 Q91902	Q91902 xenopus lae
11	294.5	31.8	717	2 P87357	P87357 brachydanio
12	294.5	31.8	720	2 Q8UMJ4	Q8UMJ4 brachydanio
13	218	23.5	772	2 Q6DI48	Q6DI48 brachydanio
14	149	16.1	802	2 Q57462	Q57462 brachydanio
15	126.5	13.7	685	1 DL14_HUMAN	Q9N616 homo sapien
16	125.5	13.7	686	1 DL14_MOUSE	Q9J171 mus musculu
17	125.5	13.6	686	2 Q9DBU9	Q9DBU9 mus musculu
18	91	9.8	364	2 Q6NM00	Q6NM00 homo sapien
19	91	9.8	364	2 Q6NM08	Q6NM08 homo sapien
20	91	9.8	364	2 CAE45875	CAE45875 homo sapi
21	91	9.8	364	2 CAE45884	CAE45884 homo sapi
22	91	9.8	364	2 CAE46001	CAE46001 homo sapi
23	88.5	9.6	1106	1 GL11_HUMAN	P08151 homo sapien
24	87.5	9.4	906	2 Q817K4	Q817K4 caenorhabdi
25	87.5	9.4	1837	2 Q95ZU1	Q95ZU1 caenorhabdi
26	87.5	9.4	1839	2 Q17383	Q17383 caenorhabdi
27	86.5	9.3	167	2 Q8CEA2	Q8CEA2 mus musculu
28	86.5	9.3	845	2 Q6XGM8	Q6XGM8 hepatitis b
29	86.5	9.3	845	2 AAP79719	AAP79719 hepatitis
30	86.5	9.3	1561	1 Y34F_DROME	Q9W5D0 drosophila
31	84.5	9.1	845	2 Q6XGM0	Q6XGM0 hepatitis b

RESULT 1				
DL11_HUMAN				
ID	DL11_HUMAN	STANDARD;	PRT;	723 AA.
AC	O00548; Q9NU41; Q9UDV2;			
DT	15-JUL-1998 (Rel. 36, Created)			
DT	15-JUL-1998 (Rel. 36, Last sequence update)			
DT	05-JUL-2004 (Rel. 44, Last annotation update)			
DE	Delta-like protein 1, precursor (Drosophila Delta homolog 1) (Delta1)			
DE	(H-Delta-1) (UNQ146/PRO172).			
GN	Name=DL11;			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=99180765; PubMed=10079256;			
RA	Gray G.E., Mann R.S., Mitsiadis E., Henrique D., Carcangiu M.-L., Banks A., Leiman J., Ward D., Ish-Horowitz D., Artavanis-Tsakonas S.;			
RT	"Human ligands of the Notch receptor."			
RL	Am. J. Pathol. 154:785-794 (1999).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RA	Han W., Ye Q., Moore M.A.S.;			
RT	"A soluble form of human delta-like-1 inhibits differentiation of hematopoietic progenitor cells."			
RL	Submitted (OCT-1999) to the EMBL/GenBank/DBSJ databases.			
RN	[3]			
RP	SEQUENCE FROM N.A.			
RA	Oda T., Chandrasekharappa S.C.;			
RT	"Human Delta 1 gene sequence."			
RL	Submitted (JAN-2000) to the EMBL/GenBank/DBSJ databases.			
RN	[4]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003;			
RA	Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J., Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P., Eaton D., Foster J., Grimaldi C., Gu Q., Hass P.E., Heldens S., Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J., Lewis L., Liao D., Mark M., Robbie E., Sanchez C., Schoenfeld J., Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A., Vandlen R., Watanabe C., Wieand D., Woods K., Xie M.-H., Yansura D., Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I., Godowski P.;			
RT	"The secreted protein discovery initiative (SPDI), a large-scale effort to identify novel human secreted and transmembrane proteins: a bioinformatics assessment."			
RL	Genome Res. 13:2265-2270 (2003).			
RN	[5]			
RP	SEQUENCE FROM N.A.			
RA	Almeida J.;			
RN	[6]			
RP	Submitted (APR-2000) to the EMBL/GenBank/DBSJ databases. FUNCTION.			

Q6XGR9 hepatitis b  
Aap79768 hepatitis  
Aap79817 hepatitis  
Q8N7X4 homo sapien  
Q86U23  
O55005 rattus norv  
Q6ZDE6 oryza sativ  
Bad09364 oryza sat  
Q8JX18 hepatitis b  
Q17652 caenorhabdi  
Q6XGR2 hepatitis b  
Aap79775 hepatitis  
Q9JNH4 mesocricetu  
Q8H077 oryza sativ

RX MEDLINE=21464863; PubMed=11581320;  
RA Taleco A.C., Neves H., Hooiberg E., Gameiro P., Clode N., Haury M.,  
RT "Differential effects of Notch ligands Delta-1 and Jagged-1 in human  
RT lymphoid differentiation.";  
RL J. Exp. Med. 194:991-1001(2001).  
CC -|- FUNCTION: Acts as a ligand for Notch receptors. Blocks the  
CC differentiation of progenitor cells into the B-cell lineage while  
CC promoting the emergence of a population of cells with the  
CC characteristics of a T-cell/NK-cell precursor.  
CC -|- SUBUNIT: Interacts with Notch receptors.  
CC -|- SUBCELLULAR LOCATION: Type I membrane protein.  
CC -|- TISSUE SPECIFICITY: Expressed in heart and pancreas, with lower  
CC expression in brain and muscle and almost no expression in  
CC placenta, lung, liver, and kidney.  
CC -|- SIMILARITY: Contains 1 DSL domain.  
CC -|- SIMILARITY: Contains 8 EGF-like domains.  
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CC -----  
DR EMBL; AF003522; AAB61286.1; -;  
DR EMBL; AF196571; AAF05834.1; -;  
DR EMBL; AF222310; AAG09716.1; -;  
DR EMBL; AF358892; AAG09251.1; -;  
DR EMBL; AL078605; CAB89569.1; -;  
DR HSSP; P00740; IEDM.  
DR Genew; HGNC:2908; DLL1.  
DR MIM; 606582; -;  
DR GO; GO:0005576; C:extracellular; NAS.  
DR GO; GO:0005887; C:integral to plasma membrane; NAS.  
DR GO; GO:0005112; F:Notch binding; IPI.  
DR GO; GO:0030154; P:cell differentiation; TAS.  
DR GO; GO:0001709; P:cell fate determination; NAS.  
DR GO; GO:0001701; P:embryonic development (sensu Mammalia); ISS.  
DR GO; GO:0009912; P:hair cell fate commitment; ISS.  
DR GO; GO:0030097; P:hemopoiesis; NAS.  
DR GO; GO:0042472; P:inner ear morphogenesis; ISS.  
DR GO; GO:0007399; P:neurogenesis; ISS.  
DR GO; GO:0007219; P:Notch signaling pathway; NAS.  
DR GO; GO:0042475; P:odontogenesis (sensu Vertebrata); ISS.  
DR GO; GO:0030155; P:regulation of cell adhesion; TAS.  
DR InterPro; IPR000152; Asx\_hydroxyl\_s.  
DR InterPro; IPR001774; DSL.  
DR InterPro; IPR000742; EGF\_2.  
DR InterPro; IPR001881; EGF\_Ca.  
DR InterPro; IPR001438; EGF\_II.  
DR InterPro; IPR006209; EGF\_like.  
DR Pfam; PF01414; DSL; 1.  
DR Pfam; PF00008; EGF; 6.  
DR PRINTS; PR00010; EGF\_BLOOD.  
DR SMART; SM00051; DSL; 1.  
DR SMART; SM00179; EGF\_CA; 4.  
DR PROSITE; PS00010; ASX\_HYDROXYL; 3.  
DR PROSITE; PS00022; EGF\_1; 8.  
DR PROSITE; PS01186; EGF\_2; 8.  
DR PROSITE; PS00026; EGF\_3; 7.  
DR PROSITE; PS01187; EGF\_CA; 1.  
DR Developmental protein; Differentiation; EGF-like domain; Glycoprotein;  
KW Repeat; Signal; Transmembrane.  
FT SIGNAL 1 17 Potential.  
FT CHAIN 18 723 Delta-like protein 1.  
FT DOMAIN 18 545 Extracellular (Potential).  
FT TRANSMEM 546 568 Potential.  
FT DOMAIN 569 723 Cytoplasmic (Potential).  
FT DOMAIN 159 221 DSL.  
FT DOMAIN 226 254 EGF-like 1.  
FT DOMAIN 257 285 EGF-like 2.

FT DOMAIN 292 325  
FT DOMAIN 332 363  
FT DOMAIN 370 402  
FT DOMAIN 409 440  
FT DOMAIN 447 478  
FT DOMAIN 485 516  
FT DISULFID 226 237  
FT DISULFID 230 243  
FT DISULFID 245 254  
FT DISULFID 257 268  
FT DISULFID 263 274  
FT DISULFID 276 285  
FT DISULFID 282 293  
FT DISULFID 298 314  
FT DISULFID 316 325  
FT DISULFID 332 343  
FT DISULFID 337 352  
FT DISULFID 354 363  
FT DISULFID 370 381  
FT DISULFID 375 391  
FT DISULFID 393 402  
FT DISULFID 409 420  
FT DISULFID 414 429  
FT DISULFID 431 440  
FT DISULFID 447 457  
FT DISULFID 459 478  
FT DISULFID 485 496  
FT DISULFID 490 505  
FT DISULFID 507 516  
FT CARBOHYD 477 477  
FT CONFLICT 498 498  
FT CONFLICT 502 502  
FT CONFLICT 510 510  
SQ SEQUENCE 723 AA; 77956 MW; B4EC455FFA32A12B CRC64;  
Query Match 57.0%; Score 527.5; DB 1; Length 723;  
Best Local Similarity 64.8%; Pred. No. 2.7e-43;  
Matches 114; Conservative 4; Mismatches 13; Indels 45; Gaps 4;  
QY 1 TNNLANCQREKDISVSIIGATGIXNTNKADFXGDXSSDKNGFKQARYPSVDYNLVQD 60  
DB 589 TNNLANCQREKDISVSIIGATGIXNTNKADF-HGDHSADKNGF-KARYPAVDYNLVQD 646  
QY 61 LKGDPTAVRTSHSKDTCQSPGSSGRRRG-PRPHSGXACCGPGSGGTGTVSSWNHCSV 119  
DB 647 LKGDPTAVRDAHSKRDTCQPGSGSGEGKPTTLRG----- 683  
QY 120 SLPKCSHAPIVDVLPFSPGEASERKRPDSCGSTSKDTKYQSVYVISEKDECVIA 175  
DB 684 -----GEASERKRPDSCGSTSKDTKYQSVYVISEKDECVIA 720  
RESULT 2  
DLL1 RAT  
ID DLL1 RAT STANDARD; PRT; 714 AA.  
AC P97677;  
DT 01-NOV-1997 (Rel. 35, Created)  
DT 01-NOV-1997 (Rel. 35, Last sequence update)  
DT 05-JUL-2004 (Rel. 44, Last annotation update)  
DE Delta-like protein 1 precursor (Drosophila Delta homolog 1) (Deltal).  
GN Name=Dll1;  
OS Rattus norvegicus (Rat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
OX NCBI\_TaxID=10116;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Disibio G., Hoshii L., Boulter J., Weinmaster G.;  
RL Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.  
CC -|- FUNCTION: May be involved in cell-to-cell communication in  
CC mammalian embryos. May have a role in cellular interactions  
CC underlying somitogenesis and development of the nervous system (By  
CC similarity).

CC -!- SUBUNIT: Interacts with Notch receptors.  
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein.  
 CC -!- SIMILARITY: Contains 1 DSL domain.  
 CC -!- SIMILARITY: Contains 8 EGF-like domains.  
 CC -----  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 CC EMBL; U78889; AAB37343.1; -;  
 CC HSP; P08709; IBF9.  
 CC RGD; 70949; D111.  
 CC GO; GO:0005576; C:extracellular; ISS.  
 CC GO; GO:0005887; C:integral to plasma membrane; ISS.  
 CC GO; GO:0005112; P:Notch binding; IPI.  
 CC GO; GO:0030154; P:cell fate determination; ISS.  
 CC GO; GO:0001709; P:cell fate determination; ISS.  
 CC GO; GO:0001701; P:embryonic development (sensu Mammalia); ISS.  
 CC GO; GO:0009912; P:hair cell fate commitment; NAS.  
 CC GO; GO:0030097; P:hemopoiesis; ISS.  
 CC GO; GO:0042472; P:inner ear morphogenesis; ISS.  
 CC GO; GO:0007399; P:neurogenesis; NAS.  
 CC GO; GO:0007219; P:Notch signaling pathway; NAS.  
 CC GO; GO:0042475; P:odontogenesis (sensu Vertebrata); ISS.  
 CC GO; GO:0030155; P:regulation of cell adhesion; ISS.  
 CC InterPro; IPR000152; Asx\_hydroxyl\_S.  
 CC InterPro; IPR001774; DSL.  
 CC InterPro; IPR000742; EGF 2.  
 CC InterPro; IPR001881; EGF\_Ca.  
 CC InterPro; IPR001438; EGF\_II.  
 CC InterPro; IPR006209; EGF\_like.  
 CC Pfam; PF01414; DSL; 1.  
 CC PRINTS; PR00008; EGF; 6.  
 CC PRINTS; PR00010; EGFBLD.  
 CC SMART; SM00051; DSL; 1.  
 CC SMART; SM00179; EGF\_CA; 4.  
 CC PROSITE; PS00010; ASX\_HYDROXYL; 3.  
 CC PROSITE; PS00022; EGF\_1; 8.  
 CC PROSITE; PS01186; EGF\_2; 8.  
 CC PROSITE; PS00026; EGF\_3; 7.  
 CC PROSITE; PS01187; EGF\_CA; 2.  
 KW Developmental protein; Differentiation; EGF-like domain; Glycoprotein;  
 KW Repeat; Signal; Transmembrane.  
 FT SIGNAL 1 17 Potential.  
 FT CHAIN 18 714 Delta-like protein 1.  
 FT DOMAIN 18 537 Extracellular (Potential).  
 FT TRANSMEM 538 560 Potential.  
 FT DOMAIN 561 744 Cytoplasmic (Potential).  
 FT DOMAIN 158 220 DSL.  
 FT DOMAIN 225 253 EGF-like 1.  
 FT DOMAIN 256 324 EGF-like 2.  
 FT DOMAIN 291 324 EGF-like 3.  
 FT DOMAIN 331 362 EGF-like 4.  
 FT DOMAIN 369 401 EGF-like 5.  
 FT DOMAIN 408 439 EGF-like 6.  
 FT DOMAIN 446 477 EGF-like 7.  
 FT DOMAIN 484 515 EGF-like 8.  
 FT DISULFID 225 236 By similarity.  
 FT DISULFID 229 242 By similarity.  
 FT DISULFID 244 253 By similarity.  
 FT DISULFID 256 267 By similarity.  
 FT DISULFID 262 273 By similarity.  
 FT DISULFID 275 284 By similarity.  
 FT DISULFID 291 303 By similarity.  
 FT DISULFID 297 313 By similarity.  
 FT DISULFID 315 324 By similarity.  
 FT DISULFID 331 342 By similarity.  
 FT DISULFID 336 351 By similarity.  
 FT DISULFID 353 362 By similarity.

FT DISULFID 369 380 By similarity.  
 FT DISULFID 374 390 By similarity.  
 FT DISULFID 392 401 By similarity.  
 FT DISULFID 408 419 By similarity.  
 FT DISULFID 413 428 By similarity.  
 FT DISULFID 430 439 By similarity.  
 FT DISULFID 446 466 By similarity.  
 FT DISULFID 468 477 By similarity.  
 FT DISULFID 484 495 By similarity.  
 FT DISULFID 489 504 By similarity.  
 FT DISULFID 506 515 By similarity.  
 FT CARBOHYD 476 476 N-linked (GlcNAc...) (Potential).  
 SQ SEQUENCE 714 AA; 77378 MW; 4B8EE272BAEA27E CRC64;  
 Query Match 48.1%; Score 445; DB 1; Length 714;  
 Best Local Similarity 54.3%; Pred. NO. 3.7e-35;  
 Matches 95; Conservative 12; Mismatches 24; Indels 44; Gaps 3;  
 QY 1 TWNNLANCOREKDISVSIIGATGIXNTNKKADFPXGDXSDXNGKGFQKARYPSVDYNLVQD 60  
 Db 581 TWNNLANCOREKDVSVSIIGATQIKNTNKKADF-HGDHGADKSSF-KARYPTVDYNLIRD 638  
 QY 61 LKGDVTAVTSHSKRDTKQSPGSGRRRGRPHSGXACGPGSGGTGWSVSNHCSVS 120  
 Db 639 LKGDVATVRDAHSKRDTKQSQSGVGEKSTSLRG----- 674  
 QY 121 LPKCSHAFIVDFLYPPFSGEASERKPDSCSTKDYQSVYVISEKDECVIA 175  
 Db 675 -----GEVDPKRKPESVYSTSKDYQSVYVLSAEKDECVIA 711  
 RESULT 3  
 O6PFV7 PRELIMINARY; PRT; 722 AA.  
 AC Q6PFV7  
 DT 05-JUL-2004 (TREMBlrel. 27, Created)  
 DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)  
 DT 01-OCT-2004 (TREMBlrel. 28, Last annotation update)  
 DE Delta-like 1.  
 GN Name=D111;  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]\_TaxID=10090;  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6; TISSUE=Mouse;  
 RX MEDLINE=2238257; PubMed=12477932;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Ussid T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
 RA Richards S., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Whiting J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
 RA Krzywinski M.I., Skalska U., Smaluk D.E., Schnerch A., Schein J.E.,  
 RA Jones S.J., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6; TISSUE=Mouse;  
 RA Strausberg R.;  
 RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.

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RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6; TISSUE=Mouse;
RA Strausberg R.;
RL Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.
[4]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J;
RA Nagaraja R., Waeltz P., Brathwaite M.E.;
RL Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.
[5]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J;
RA Brathwaite M., Waeltz P., Dudekula D., Nagaraja R.;
RL Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.
CC -I- SIMILARITY: Contains 8 EGF-like domains.
DR EMBL; BC057400; AAH57400.1; -.
DR EMBL; BC065063; AAH65063.1; -.
DR EMBL; AY97019; AAR30869.1; -.
DR GO; GO:000515; F:protein binding; IPI.
DR GO; GO:0007386; P:compartment specification; IMP.
DR GO; GO:0007368; P:determination of left/right symmetry; IMP.
DR GO; GO:001757; P:somite specification; IMP.
DR InterPro; IPR000152; Axx_hydroxyl_s.
DR InterPro; IPR001774; DSL.
DR InterPro; IPR000742; EGF_2.
DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR001438; EGF_II.
DR InterPro; IPR006209; EGF_like.
DR InterPro; IPR006210; IEGF.
DR Pfam; PF01414; DSL; 1.
DR Pfam; PF00008; EGF; 6.
DR Pfam; PF07645; EGF_CA; 1.
DR PRINTS; PR00010; EGFBL00D.
DR SMART; SM00051; DSL; 1.
DR SMART; SM00181; EGF; 8.
DR SMART; SM00179; EGF_CA; 6.
DR PROSITE; PS00010; ASX_HYDROXYL; 3.
DR PROSITE; PS00022; EGF_1; 8.
DR PROSITE; PS01186; EGF_2; 8.
DR PROSITE; PS50026; EGF_3; 6.
DR PROSITE; PS01187; EGF_CA; 2.
KW EGF-like domain.
SQ SEQUENCE 722 AA; 78449 MW; 9D570B9DC7EEC75E CRC64;

Query Match 46.5%; Score 431; DB 2; Length 722;
Best Local Similarity 53.7%; Pred. No. 9.1e-34;
Matches 94; Conservative 13; Mismatches 24; Indels 44; Gaps 4;

QY 1 TNNLANCOREKDISVSIIGATGIXNTNKKADFPXGDXSDKNGFOKARYPSVDYNLVQD 60
DB 589 TNNLANCOREKDVSVSIIGATQIKNTNKKADP-HGDHGAEKSSF-KVRYPTVDYNLVRD 646

QY 61 LKGDDTAVRTSHSKRTKQSPGSGRRRPRPHSGXACCGPGSGGTGWSVSNHCSVS 120
DB 647 LKGDATVDRTHSKRTKQSSAGEEK-----IAPTLRG----- 682

QY 121 LPKCSHAFIVDFLYPFPFSGEASERKPDSCGCTSKDTKYQSVYVISEKDECVIA 175
DB 683 -----GEIPDKRPESVYSTSKDTKYQSVVYLSAEKDECVIA 719

RESULT 5
AAR30869 PRELIMINARY; PRT; 722 AA.
ID AAR30869
AC AAR30869;
DT 02-MAR-2004 (TREMBLrel. 27, Created)
DT 02-MAR-2004 (TREMBLrel. 27, Last sequence update)
DT 02-MAR-2004 (TREMBLrel. 27, Last annotation update)
DE Delta like-1.
GN DLL1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J;
RA Nagaraja R., Waeltz P., Brathwaite M.E.;
RT "Genomic Sequence Analysis in the Mouse t-complex Region.";
RL Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.
[2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J;
RA Brathwaite M., Waeltz P., Dudekula D., Nagaraja R.;
```

[illegible]

```

DR InterPro; IPR000742; EGF_2.
DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR001438; EGF_II.
DR InterPro; IPR006209; EGF_like.
DR Pfam; PF01414; DSL; 1.
DR Pfam; PF00008; EGF; 6.
DR PRINTS; PR00010; EGFBLD.
DR PROSITE; PS00010; ASX_HYDROXYL; 3.
DR PROSITE; PS00022; EGF_1; 8.
DR PROSITE; PS01186; EGF_2; 8.
DR PROSITE; PS00026; EGF_3; 7.
DR PROSITE; PS01187; EGF_CA; 2.
KW Developmental protein; Differentiation; EGF-like domain; Glycoprotein;
KW Repeat; Signal; Transmembrane.
FT SIGNAL 1 17 Potential.
FT CHAIN 18 722 Delta-like protein 1.
FT DOMAIN 18 545 Extracellular (Potential).
FT TRANSMEM 545 568 Potential.
FT DOMAIN 569 722 Cytoplasmic (Potential).
FT DOMAIN 158 220 DSL.
FT DOMAIN 225 253 EGF-like 1.
FT DOMAIN 256 284 EGF-like 2.
FT DOMAIN 291 324 EGF-like 3.
FT DOMAIN 331 362 EGF-like 4, calcium-binding (Potential).
FT DOMAIN 369 401 EGF-like 5.
FT DOMAIN 408 439 EGF-like 6.
FT DOMAIN 446 477 EGF-like 7, calcium-binding (Potential).
FT DOMAIN 484 515 EGF-like 8.
FT DISULFID 225 236 By similarity.
FT DISULFID 229 242 By similarity.
FT DISULFID 244 253 By similarity.
FT DISULFID 256 267 By similarity.
FT DISULFID 262 273 By similarity.
FT DISULFID 275 284 By similarity.
FT DISULFID 291 303 By similarity.
FT DISULFID 297 313 By similarity.
FT DISULFID 315 324 By similarity.
FT DISULFID 331 342 By similarity.
FT DISULFID 336 351 By similarity.
FT DISULFID 353 362 By similarity.
FT DISULFID 369 380 By similarity.
FT DISULFID 374 390 By similarity.
FT DISULFID 392 401 By similarity.
FT DISULFID 408 419 By similarity.
FT DISULFID 413 428 By similarity.
FT DISULFID 430 439 By similarity.
FT DISULFID 446 466 By similarity.
FT DISULFID 468 477 By similarity.
FT DISULFID 484 495 By similarity.
FT DISULFID 489 504 By similarity.
FT DISULFID 506 515 By similarity.
FT CARBOHYD 476 476 N-linked (GlcNAc...) (Potential).
SQ SEQUENCE 722 AA; 78448 MW; 95F581B56DCEC9B0 CRC64;

Query Match 46.2%; Score 428; DB 1; Length 722;
Best Local Similarity 53.7%; Pred. No. 1.8e-33;
Matches 94; Conservative 12; Mismatches 25; Indels 44; Gaps 4;

QY 1 TWNNLANCOREKDISVSIIGATGIXNTNKKADFPXGDXSSDKNGFQKARYPSVDYNLVQD 60
DB TWNNLANCOREKDVSVSIIGATQIKNTNKKADFP-HGDHGAKKSF-KVRYPTVDYNLVQD 646

QY 61 LKGDPTAVRTSHSKRDTKQSPGSGRRRPRPHSGXACCGPGSGGTGWGSSWNHCYSV 120
DB LKGDPTAVRTSHSKRDTKQSPGSGRRRPRPHSGXACCGPGSGGTGWGSSWNHCYSV 682

QY 121 LPKCSHAFIVDFLYPFPSGEASERKPDSCSTKDTKYQSVYVISEEKDECVIA 175
DB LKGDPTAVRTSHSKRDTKQSPGSGRRRPRPHSGXACCGPGSGGTGWGSSWNHCYSV 683

Query Match 46.2%; Score 428; DB 1; Length 722;
Best Local Similarity 53.7%; Pred. No. 1.8e-33;
Matches 94; Conservative 12; Mismatches 25; Indels 44; Gaps 4;

QY 1 TWNNLANCOREKDISVSIIGATGIXNTNKKADFPXGDXSSDKNGFQKARYPSVDYNLVQD 60
DB TWNNLANCOREKDVSVSIIGATQIKNTNKKADFP-HGDHGAKKSF-KVRYPTVDYNLVQD 646

QY 61 LKGDPTAVRTSHSKRDTKQSPGSGRRRPRPHSGXACCGPGSGGTGWGSSWNHCYSV 120
DB LKGDPTAVRTSHSKRDTKQSPGSGRRRPRPHSGXACCGPGSGGTGWGSSWNHCYSV 682

QY 121 LPKCSHAFIVDFLYPFPSGEASERKPDSCSTKDTKYQSVYVISEEKDECVIA 175
DB LKGDPTAVRTSHSKRDTKQSPGSGRRRPRPHSGXACCGPGSGGTGWGSSWNHCYSV 683

RESULT 8
Q90656

```



```

OX NCBI_TaxID=8330;
RN [1]
RP SEQUENCE FROM N.A.
RA Nakamura K., Kikuchi Y., Susaki K., Chiba C., Saito T.;
RL Submitted (Oct-2002) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Contains 8 EGF-like domains.
DR EMBL; AB095017; BAC41350.2; -.
DR HSSP; P00740; 1EDM.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005509; F:calcium ion binding; IEA.
DR GO; GO:0007154; P:cell communication; IEA.
DR InterPro; IPR000152; Asx_hydroxyl_S.
DR InterPro; IPR000742; EGF 2.
DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR001438; EGF_II.
DR InterPro; IPR006209; EGF_like.
DR Pfam; PF01414; DSL; 1.
DR Pfam; PF00008; EGF; 6.
DR PRINTS; PR00010; EGFBL00D.
DR SMART; SM00051; DSL; 1.
DR SMART; SM00179; EGF_CA; 4.
DR PROSITE; PS00010; ASX_HYDROXYL; 3.
DR PROSITE; PS00022; EGF_1; 8.
DR PROSITE; PS01186; EGF_2; 7.
DR PROSITE; PS00026; EGF_3; 6.
DR PROSITE; PS01187; EGF_CA; 2.
KW EGF-like domain.
SQ SEQUENCE 726 AA; 7986 MW; 352A40219AE67F41 CRC64;

Query Match 41.8%; Score 387.5; DB 2; Length 726;
Best Local Similarity 50.3%; Pred. No. 1.8e-29;
Matches 88; Conservative 17; Mismatches 25; Indels 45; Gaps 5;

QY 1 TNNLANCOREKDISVSIIGATGIXNTNKKADFXKDXSSDKNGFKQARYPSVDYNLVOD 60
DB TNNLANCOREKDISVSIIGATGIXNTNKKADL-YSEISDKNGY-KARYPSVDYNLVHE 551
QY 61 LKGDVTAVRTSHSKRDITKQSPGSGRRRGRPHSGACCGPGSGGTGWGWSNHCVS 120
DB LKHED-SVKEEHGKRESKCIANGSEAKHP-----VQ 683
QY 121 LPKCSHAFIVDLYPPFSGEASERKPDSCGTSKDTKYQSVYVISEEKDECVIA 175
DB LK-----SSETSERRPESLYSTSKETKYQSVYVISEAKDECIIA 723

RESULT 10
Q91902 PRELIMINARY; PRT; 721 AA.
AC Q91902;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE X-Delta-1.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95319507; PubMed=7596411;
RA Henrique D., Adam J., Myat A., Chitnis A., Lewis J., Ish-Horowicz D.;
RT "Expression of a Delta homologue in prospective neurons in the chick."
RL Nature 375:787-790(1995).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=95319503; PubMed=7596407;
RA Chitnis A., Henrique D., Lewis J., Ish-Horowicz D., Kintner C.;

"Primary neurogenesis in Xenopus embryos regulated by a homologue of the Drosophila neurogenic gene Delta.";
Nature 375:761-766(1995).
EMBL; I42229; AAC38017.1; -.
DR HSSP; P00740; 1EDM.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005509; F:calcium ion binding; IEA.
DR GO; GO:0007154; P:cell communication; IEA.
DR InterPro; IPR000152; Asx_hydroxyl_S.
DR InterPro; IPR001774; DSL.
DR InterPro; IPR000742; EGF 2.
DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR001438; EGF_II.
DR InterPro; IPR006209; EGF_like.
DR Pfam; PF01414; DSL; 1.
DR Pfam; PF00008; EGF; 6.
DR PRINTS; PR00010; EGFBL00D.
DR SMART; SM00051; DSL; 1.
DR SMART; SM00179; EGF_CA; 4.
DR PROSITE; PS00010; ASX_HYDROXYL; 3.
DR PROSITE; PS00022; EGF_1; 8.
DR PROSITE; PS01186; EGF_2; 8.
DR PROSITE; PS00026; EGF_3; 6.
DR PROSITE; PS01187; EGF_CA; 2.
KW EGF-like domain.
SQ SEQUENCE 721 AA; 79922 MW; 9EBDC85C439DD194 CRC64;

Query Match 38.4%; Score 356; DB 2; Length 721;
Best Local Similarity 46.3%; Pred. No. 2.3e-26;
Matches 81; Conservative 15; Mismatches 33; Indels 46; Gaps 4;

QY 1 TNNLANCOREKDISVSIIGATGIXNTNKKADFXKDXSSDKNGFKQARYPSVDYNLVOD 60
DB TNNLANCOREKDISVSIIGTQIKNTNKKIDF-LSESNNEKNGI-KRYPSPDYNLVHE 647
QY 61 LKGDVTAVRTSHSKRDITKQSPGSGRRRGRPHSGACCGPGSGGTGWGWSNHCVS 120
DB LKNEESP-KEERSKCEAKSSNDSSE----- 673
QY 121 LPKCSHAFIVDLYPPFSGEASERKPDSCGTSKDTKYQSVYVISEEKDECVIA 175
DB -----DVNSVHSKRDSERRRRPDSAVSTSKDTKYQSVYVISEKDECIIA 718

RESULT 11
P87357 PRELIMINARY; PRT; 717 AA.
AC P87357;
DT 01-MAY-1997 (TREMBLrel. 03, Created)
DT 01-MAY-1997 (TREMBLrel. 03, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE Deltad transmembrane protein precursor.
GN Name=dld; Synonyms=deltad;
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97346722; PubMed=9203139;
RA Dornseifer P., Takke C., Campos-Ortega J.A.;
RT "Overexpression of a zebrafish homologue of the Drosophila neurogenic gene delta perturbs differentiation of primary neurons and somitic development."
RL Mech. Dev. 63:159-171(1997).
DR EMBL; Y11760; CAA72425.1; -.
DR HSSP; P00740; 1EDM.
DR ZFIN; ZDB-GENE-950415-47; dld.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0005509; F:calcium ion binding; IEA.
DR GO; GO:0007154; P:cell communication; IEA.
DR InterPro; IPR000152; Asx_hydroxyl_S.

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DR InterPro; IPR001774; DSL.
DR InterPro; IPR000742; EGF_2.
DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR001438; EGF_II.
DR InterPro; IPR006209; EGF_like.
DR Pfam; PF01414; DSL; 1.
DR Pfam; PF00008; EGF; 6.
DR PRINTS; PR00010; EGFBL00D.
DR SMART; SM00051; DSL; 1.
DR SMART; SM00179; EGF_Ca; 4.
DR PROSITE; PS00010; ASX_HYDROXYL; 3.
DR PROSITE; PS00022; EGF_1; 8.
DR PROSITE; PS01186; EGF_2; 8.
DR PROSITE; PS00026; EGF_3; 6.
DR PROSITE; PS01187; EGF_Ca; 2.
DR PROSITE; PS01187; EGF_Ca; 2.
KW EGF-like domain; Signal; Transmembrane.
FT SIGNAL 4 11 Potential.
SQ SEQUENCE 717 AA; 79061 MW; 9C5A0162504593E4 CRC64;

Query Match 31.8%; Score 294.5; DB 2; Length 717;
Best Local Similarity 42.0%; Pred. No. 2.7e-20;
Matches 74; Conservative 14; Mismatches 37; Indels 51; Gaps 7;

QY 1 TNNNLANCO-REKDISVSIIGATGIXNTNKKADFXKDXSSDKNGFQKARYPSVDYNLVQ 59
Db 589 TNNNLNRRSREKDLVSIIIGATQVNIKKVDF---QSDGDKNGF-KSRYSLVDYNLVH 644
QY 60 DLKGDPTAVRTSHSKRDTKCQSPGSGRRRPRPHSGXACCGPGSGGTGWVSSMNHCSV 119
Db 645 ELKQEDLGKEDSRSEATKCEPLDSDSEK-----HR-----NH--- 678
QY 120 SLPKCSHAFIVDFLYFPFSGEASERKPDSCGTSKDTKYQSVYVISEKDECVIA 175
Db 679 -----LKSDDSRKRTESLC---KDTKYQSVFVLSSEKDECIIA 714

RESULT 13
Q8DI48 PRELIMINARY; PRT; 772 AA.
AC Q6DI48;
DT 01-OCT-2004 (TrEMBLrel. 28, Created)
DT 01-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 01-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Hypothetical protein.
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalek U., Smalusz D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RA Strausberg R.;
RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC075742; AAH75742.1; -.
KW Hypothetical protein.
SQ SEQUENCE 772 AA; 84968 MW; 716A014158938576 CRC64;

Query Match 23.5%; Score 218; DB 2; Length 772;
Best Local Similarity 35.0%; Pred. No. 1.1e-12;
Matches 70; Conservative 24; Mismatches 70; Indels 36; Gaps 9;

```



CC -I- SIMILARITY: Contains 8 EGF-like domains.  
CC -----  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC -----

DR ENBL; AF253468; AAF76427.1; -  
DR ENBL; AB036931; BAB16085.1; -  
DR ENBL; AB043894; BAB18581.1; -  
DR ENBL; AY358894; AAO89253.1; -  
DR ENBL; AF279305; AAF81912.1; -  
DR PIR; JC7570; JC7570.  
DR HSSP; P00740; 1EDM.  
DR Genew; HGNC:2910; DLL4.  
DR MIM; 605185; -  
DR GO; GO:0005112; F-Notch binding; TAS.  
DR GO; GO:0008015; P-circulation; TAS.  
DR GO; GO:0007165; P-signal transduction; TAS.  
DR InterPro; IPR000152; Aex\_hydroxyl\_S.  
DR InterPro; IPR001774; DSL.  
DR InterPro; IPR000742; EGF\_2.  
DR InterPro; IPR001438; EGF-II.  
DR InterPro; IPR006209; EGF\_like.  
DR Pfam; PF01414; DSL; 1.  
DR Pfam; PF00008; EGF; 7.  
DR PRINTS; PR00010; EGFBL00D.  
DR PROSITE; PS00010; ASX\_HYDROXYL; 1.  
DR PROSITE; PS00022; EGF\_1; 8.  
DR PROSITE; PS01186; EGF\_2; 7.  
DR PROSITE; PS00026; EGF\_3; 8.  
KW Developmental protein; Differentiation; Direct protein sequencing;  
KW EGF-like domain; Glycoprotein; Repeat; Signal; Transmembrane.

FT CHAIN 1 26  
FT SIGNAL 1 26  
FT CHAIN 27 685  
FT DOMAIN 27 529  
FT TRANSMEM 530 550  
FT DOMAIN 551 685  
FT DOMAIN 155 217  
FT DOMAIN 218 251  
FT DOMAIN 252 282  
FT DOMAIN 284 322  
FT DOMAIN 324 360  
FT DOMAIN 362 400  
FT DOMAIN 402 438  
FT DOMAIN 440 476  
FT DOMAIN 480 518  
FT DISULFID 222 233  
FT DISULFID 226 239  
FT DISULFID 241 250  
FT DISULFID 253 264  
FT DISULFID 259 270  
FT DISULFID 272 281  
FT DISULFID 288 300  
FT DISULFID 294 310  
FT DISULFID 312 321  
FT DISULFID 328 339  
FT DISULFID 333 348  
FT DISULFID 350 359  
FT DISULFID 365 377  
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FT DISULFID 390 399  
FT DISULFID 406 417  
FT DISULFID 411 426  
FT DISULFID 428 437  
FT DISULFID 444 454  
FT DISULFID 466 475  
FT DISULFID 484 495  
FT DISULFID 489 506  
FT DISULFID 508 517

FT CARBOHYD 108 108 N-linked (GlcNAc...) (Potential).  
FT CARBOHYD 183 183 N-linked (GlcNAc...) (Potential).  
FT CARBOHYD 205 205 N-linked (GlcNAc...) (Potential).  
FT CARBOHYD 393 393 N-linked (GlcNAc...) (Potential).  
SQ SEQUENCE 685 AA; 74604 MW; 6CF89D3C220ACC89 CRC64;  
Query Match 13.7%; Score 126.5; DB 1; Length 685;  
Best Local Similarity 26.7%; Pred. No. 0.001;  
Matches 47; Conservative 23; Mismatches 43; Indels 63; Gaps 7;  
QY 2 MNLANCOREKDISVSIIGATGIXNTNKKADFXKGDSSDKNGFQKARVPSVDYNLVQDL 61  
DB 568 MNLSDFQD-----NLIPAAQLKNTNQKKELEV-DCGLDKSNCGKQOHTLDYNL----- 617  
QY 62 KGDDTAVRTSHSKRDTKQSPGSSGR--RRGPRPHSGXACCGPGSGGTGWTGVSSMNCVS 119  
DB 618 -----APGLRGRTMPGKFPFHSKSL-----GEKAPLRLHS 648  
QY 120 SLPKCSHAFIVDFLYFPFSGEASERKRPDSGCGSTSKDTKYQSVYVISEKDECVIA 175  
DB 649 EKPEC-----RISAICS-PRDSMYQSVCLISERNECVIA 682

Search completed: December 2, 2004, 04:01:22  
Job time: 196 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 2, 2004, 03:52:42 ; Search time 39 Seconds  
(without alignments)  
431.742 Million cell updates/sec

Title: US-09-783-931-23

Perfect score: 926

Sequence: 1 TNNLANCQREKDISVSIIG.....DTKYQSVYVISEKDECVIA 175

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR\_79:\*

1: Pir1:\*

2: Pir2:\*

3: Pir3:\*

4: Pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	428	46.2	722	I48324	DELTA-like 1 - mou
2	388	41.9	728	I50719	C-Delta-1 - chicke
3	126.5	13.7	685	JC7570	Delta-4 protein -
4	125.5	13.6	686	JC7569	transforming prote
5	88.5	9.6	1106	TVHUGL	hypothetical prote
6	87.5	9.4	925	T29111	hypothetical prote
7	86.5	9.3	504	T13475	transmembrane rece
8	83.5	9.0	1651	T14160	hypothetical prote
9	83	9.0	1707	T18951	probable primase y
10	81	8.7	763	AC0108	heterogeneous ribo
11	79.5	8.6	326	A41732	snRNP-associated p
12	79.5	8.6	386	S22315	receptor-like prot
13	78.5	8.5	512	T47793	hypothetical prote
14	77.5	8.4	538	T43418	transcription fact
15	77.5	8.4	929	C96623	hypothetical prote
16	77.5	8.4	2148	A56011	transcription fact
17	75.5	8.2	263	F84849	hypothetical prote
18	75.5	8.2	435	D41602	transcription fact
19	75.5	8.2	1191	T13850	gene u-shaped prot
20	75.5	8.2	1433	A46053	bullous pemphigoid
21	75.5	8.2	1612	T30805	dutt1 protein - mo
22	75	8.1	424	T41449	probable phd finge
23	75	8.1	439	A48099	transcription fact
24	74.5	8.0	282	S78141	ribosomal protein
25	74	8.0	367	AD0404	probable sugar ABC
26	74	8.0	1464	S58984	development protei
27	74	8.0	1613	T06678	hypothetical prote
28	73.5	7.9	154	A33896	isotocin 1 / neuro
29	73.5	7.9	376	G96579	hypothetical prote

30	73	7.9	569	1	KRMSE1	keratin, 59K type
31	73	7.9	570	2	S07330	keratin, epidemal
32	73	7.9	2493	2	A55481	adenylate cyclase
33	72.5	7.8	455	2	S46033	probable membrane
34	72.5	7.8	1135	2	T42368	DNA-directed RNA p
35	72	7.8	305	2	S41860	gene Nkx-1.1 prote
36	72	7.8	843	1	JDVLJ1	DNA-directed DNA p
37	72	7.8	1611	2	T06677	hypothetical prote
38	71.5	7.7	309	2	T19389	hypothetical prote
39	71.5	7.7	677	2	H84382	gelation factor -
40	71.5	7.7	857	1	S05943	heterodisulfide re
41	71.5	7.7	1173	2	T31421	C-terminal domain-
42	71	7.7	159	2	I51077	isotocin-1 precurs
43	71	7.7	219	2	T27105	hypothetical prote
44	71	7.7	471	2	T33997	hypothetical prote
45	71	7.7	624	2	T04843	hypothetical prote

ALIGNMENTS

RESULT 1

I48324

DELTA-like 1 - mouse

C:Species: Mus musculus (house mouse)

C:Date: 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change 09-Jul-2004

C:Accession: I48324

R:Bettenhausen, B.; de Angelis, M.H.; Simon, D.; Guenet, J.L.; Gossler, A.

Development 121, 2407-2418, 1995

A:Title: Transient and restricted expression during mouse embryogenesis of Dll1, a murine

A:Reference number: I48324; MUID:95401858; PMID:7671806

A:Accession: I48324

A>Status: preliminary; translated from GB/EMBL/DBDJ

A:Molecule type: mRNA

A:Residues: 1-722 <RES>

A:Cross-References: UNIPROT:Q61483; EMBL:X80903; NID:g806569; PIDN:CAA56865.1; PID:g8065

C:Genetics:

A:Gene: Dll1

C:Superfamily: delta-4 protein; EGF homology

F:331-362/Domain: EGF homology <EGF2>

F:446-477/Domain: EGF homology <EGF>

F:484-515/Domain: EGF homology <EGF1>

Query Match	46.2%;	Score 428;	DB 2;	Length 722;
Best Local Similarity	53.7%;	Pred. No. 98-34;		
Matches	94;	Conservative 12;	Mismatches 25;	Indels 44; Gaps 4;
Qy	1	TNNLANCQREKDISVSIIGATGIXNTNKKADFXGDXSSDKNGFKQARYPSVDYNLQD	60	
Db	589	TNNLANCQREKDVSVSIIGATGIXNTNKKADF-HGDHGAKKSSF-KVRYPTVDYNLVRD	646	
Qy	61	LKGDVTAVTSHSKRDTKQSPGSSGRRRGRPHSGXACCGPGSGGTGVSNNHCSVS	120	
Db	647	LKGDVTAVTSHSKRDTKQSPGSSGRRRGRPHSGXACCGPGSGGTGVSNNHCSVS	120	
Qy	121	LPKCSHAFIVDLYFPFSGEASERKRPDSGCSKDTKYQSVYVISEKDECVIA	175	
Db	683	LPKCSHAFIVDLYFPFSGEASERKRPDSGCSKDTKYQSVYVISEKDECVIA	175	

RESULT 2

I50719

C-Delta-1 - chicken

C:Species: Gallus gallus (chicken)

C:Date: 13-Sep-1996 #sequence\_revision 13-Sep-1996 #text\_change 09-Jul-2004

C:Accession: I50719

R:Henrique, D.; Adam, J.; Myat, A.; Chitnise, A.; Lewis, J.; Ish-Horowitz, D.

Nature 375, 787-790, 1995

A:Title: Expression of a Delta homologue in prospective neurons in the chick.

A:Reference number: I50719; MUID:95319507; PMID:7596411

A:Accession: I50719

A>Status: preliminary; translated from GB/EMBL/DBDJ

A:Molecule type: mRNA

A;Residues: 1-728 <EN>  
A;Cross-references: UNIPROT:Q90656; EMBL:U26590; NID:9882411; PIDN:AAC59689.1; PID:98824  
C;Superfamily: Delta-4 protein; EGF homology  
F;299-332/Domain: EGF homology <EGX1>  
F;339-370/Domain: EGF homology <EGF1>  
F;416-447/Domain: EGF homology <EGX2>  
F;454-485/Domain: EGF homology <EGF>  
F;492-523/Domain: EGF homology <EGF3>

Query Match 41.9%; Score 388; DB 2; Length 728;  
Best Local Similarity 49.7%; Pred. No. 7.2e-30;  
Matches 87; Conservative 15; Mismatches 27; Indels 46; Gaps 5;

QY 1 TNNLANCOREKDISVSIIGATGIXNTNKKADPFXXGDXSDKNGFQKARYPSVDYNLVOD 60  
Db TNNLANCOREKDISVSIIGATGIXNTNKKADPFXXGDXSDKNGFQKARYPSVDYNLVOD 60  
QY 597 TNNLANCOREKDISVSIIGATGIXNTNKKADPFXXGDXSDKNGFQKARYPSVDYNLVOD 61  
Db TNNLANCOREKDISVSIIGATGIXNTNKKADPFXXGDXSDKNGFQKARYPSVDYNLVOD 61  
QY 61 LGDDTAVRTSHSKRDTCQSPGSSRRRGRPRPHSGXACCGPGSGGTGWGVSSWNHCSVS 120  
Db LGDDTAVRTSHSKRDTCQSPGSSRRRGRPRPHSGXACCGPGSGGTGWGVSSWNHCSVS 120  
QY 654 LKNEED-SVKEEHGKCAKETDYSEAEKS-----AVQ 685  
Db LKNEED-SVKEEHGKCAKETDYSEAEKS-----AVQ 685  
QY 121 LPKCSHAFIVDFLYFPFSGEASERKRPDSCGSTSKDTKYQSVYVISEEKDECVIA 175  
Db LPKCSHAFIVDFLYFPFSGEASERKRPDSCGSTSKDTKYQSVYVISEEKDECVIA 175  
QY 686 LK-----SSDTSERKPDVSYSTSKDTKYQSVYVISEEKDECVIA 725  
Db LK-----SSDTSERKPDVSYSTSKDTKYQSVYVISEEKDECVIA 725

RESULT 3  
JC7570  
Delta-4 protein - human  
C;Species: Homo sapiens (man)  
C;Date: 30-Jun-2001 #sequence\_revision 30-Jun-2001 #text\_change 09-Jul-2004  
R;Yoneya, T.; Tahara, T.; Nagao, K.; Yamada, Y.; Yamamoto, T.; Osawa, M.; Miyatani, S.; J. Biochem. 129, 27-34, 2001  
A;Title: Molecular cloning of Delta-4, a new mouse and human notch ligand.  
A;Reference number: JC7569, MUID: 21064937; PMID:11134954  
A;Accession: JC7570  
A;Molecule type: mRNA  
A;Residues: 1-685 <YON>  
A;Cross-references: UNIPROT:Q9NR61; DBJ:AB043894  
C;Comment: This protein, a member of the Notch family of proteins, is a transmembrane receptor that mediates the Notch signaling, the growth or differentiation of vascular endothelial cells.  
C;Genetics:  
A;Gene: delta-4  
C;Superfamily: delta-4 protein; EGF homology  
C;Keywords: transmembrane protein

Query Match 13.7%; Score 126.5; DB 2; Length 685;  
Best Local Similarity 26.7%; Pred. No. 0.0002;  
Matches 47; Conservative 23; Mismatches 43; Indels 63; Gaps 7;

QY 2 MNLANCOREKDISVSIIGATGIXNTNKKADPFXXGDXSDKNGFQKARYPSVDYNLVODL 61  
Db MNLANCOREKDISVSIIGATGIXNTNKKADPFXXGDXSDKNGFQKARYPSVDYNLVODL 61  
QY 62 KGDDTAVRTSHSKRDTCQSPGSSRRRGRPRPHSGXACCGPGSGGTGWGVSSWNHCSVS 119  
Db KGDDTAVRTSHSKRDTCQSPGSSRRRGRPRPHSGXACCGPGSGGTGWGVSSWNHCSVS 119  
QY 618 -----APGLGRGTMPKFPFPHSDKSL-----GEKAPLRLHS 648  
Db -----APGLGRGTMPKFPFPHSDKSL-----GEKAPLRLHS 648  
QY 120 SLPKCSHAFIVDFLYFPFSGEASERKRPDSCGSTSKDTKYQSVYVISEEKDECVIA 175  
Db SLPKCSHAFIVDFLYFPFSGEASERKRPDSCGSTSKDTKYQSVYVISEEKDECVIA 175  
QY 649 ERPEC-----RISAICS-PRDSMYQSVCLISEERNECVIA 682  
Db ERPEC-----RISAICS-PRDSMYQSVCLISEERNECVIA 682

RESULT 4  
JC7569  
Delta-4 protein - mouse  
C;Species: Mus musculus (house mouse)  
C;Date: 30-Jun-2001 #sequence\_revision 30-Jun-2001 #text\_change 09-Jul-2004  
R;Yoneya, T.; Tahara, T.; Nagao, K.; Yamada, Y.; Yamamoto, T.; Osawa, M.; Miyatani, S.; J. Biochem. 129, 27-34, 2001  
A;Title: Molecular cloning of Delta-4, a new mouse and human notch ligand.

A;Reference number: JC7569; MUID: 21064937; PMID:11134954  
A;Accession: JC7569  
A;Molecule type: mRNA  
A;Residues: 1-686 <YON>  
A;Cross-references: UNIPROT:Q9DBU9; DBJ:AB043893  
C;Comment: This protein, a member of the Notch family of proteins, is a transmembrane receptor that mediates the Notch signaling, the growth or differentiation of vascular endothelial cells.  
C;Genetics:  
A;Gene: delta-4  
C;Superfamily: delta-4 protein; EGF homology

Query Match 13.6%; Score 125.5; DB 2; Length 686;  
Best Local Similarity 24.9%; Pred. No. 0.00025;  
Matches 44; Conservative 25; Mismatches 43; Indels 65; Gaps 6;

QY 2 MNLANCOREKDISVSIIGATGIXNTNKKADPFXXGDXSDKNGFQKARYPSVDYNLVODL 61  
Db MNLANCOREKDISVSIIGATGIXNTNKKADPFXXGDXSDKNGFQKARYPSVDYNLVODL 61  
QY 62 KGDDTAVRTSHSKRDTCQSPGSSRRRGRPRPHSGXACCGPGSGGTGWGVSSWNHCSVS 121  
Db KGDDTAVRTSHSKRDTCQSPGSSRRRGRPRPHSGXACCGPGSGGTGWGVSSWNHCSVS 121  
QY 623 LG-----RGMPGKYPHSDKS-----LGEKV 643  
Db LG-----RGMPGKYPHSDKS-----LGEKV 643  
QY 122 PKCSHAFIVDFLYFPFSGEASERKRPD-----SGCSTSKDTKYQSVYVISEEKDECVIA 175  
Db PKCSHAFIVDFLYFPFSGEASERKRPD-----SGCSTSKDTKYQSVYVISEEKDECVIA 175  
QY 644 PLRLHS-----EKPECRISAICPRDSMYQSVCLISEERNECVIA 683  
Db PLRLHS-----EKPECRISAICPRDSMYQSVCLISEERNECVIA 683

RESULT 5  
TVHUGL  
transforming protein gli - human  
N;Alternate names: glioma-associated transforming protein  
C;Species: Homo sapiens (man)  
C;Date: 31-Mar-1991 #sequence\_revision 31-Mar-1991 #text\_change 09-Jul-2004  
C;Accession: S00672  
R;Kinzler, K.W.; Ruppert, J.M.; Bigner, S.H.; Vogelstein, B. Nature 352, 371-374, 1988  
A;Title: The GLI gene is a member of the Kruppel family of zinc finger proteins.  
A;Reference number: S00672; MUID:88175051; PMID:2832761  
A;Accession: S00672  
A;Molecule type: mRNA  
A;Residues: 1-1106 <KN>  
A;Cross-references: UNIPROT:P08151; EMBL:X07384; NID:g31767; PIDN:CAA30297.1; PID:g31768  
C;Genetics:  
A;Gene: GDB:GLI  
A;Cross-references: GDB:119988; OMIM:165220  
A;Map position: 12q13.2-12q13.3  
C;Superfamily: gli transforming protein  
C;Keywords: DNA binding; duplication; oncogene; transcription regulation; transforming protein  
F;235-260/Region: zinc finger CCHH motif  
F;268-295/Region: zinc finger CCHH motif  
F;301-325/Region: zinc finger CCHH motif  
F;331-356/Region: zinc finger CCHH motif  
F;362-387/Region: zinc finger CCHH motif

Query Match 9.6%; Score 88.5; DB 1; Length 1106;  
Best Local Similarity 21.8%; Pred. No. 1.7;  
Matches 42; Conservative 24; Mismatches 62; Indels 65; Gaps 8;

QY 39 SSDKNGFQKARYPSVDYNLVODLKGPD-TFVARTSHSKR-----DTKCQSPGSS----- 85  
Db SSDKNGFQKARYPSVDYNLVODLKGPD-TFVARTSHSKR-----DTKCQSPGSS----- 85  
QY 86 -----GRRRGRPHSGXACCGP-GSGGTGWGVSSWNHCSVSLPKCSHAFIVDFL 133  
Db -----GRRRGRPHSGXACCGP-GSGGTGWGVSSWNHCSVSLPKCSHAFIVDFL 133  
QY 129 MSPSLGFFPAQNMHQKGPSPFVGQPCGPHDSARG--GMIPHPQSRGPFPTCOLKSELDM 186  
Db MSPSLGFFPAQNMHQKGPSPFVGQPCGPHDSARG--GMIPHPQSRGPFPTCOLKSELDM 186  
QY 134 Y-----FPFSGAS-----ERKPEDS-----GCSTSK 155  
Db Y-----FPFSGAS-----ERKPEDS-----GCSTSK 155  
QY 187 VGKCRPEPLEGDMSPNSTGIQDPLLGLMDGREDLEREEKREPESVYETDCRDWDCSQEF 246  
Db VGKCRPEPLEGDMSPNSTGIQDPLLGLMDGREDLEREEKREPESVYETDCRDWDCSQEF 246  
QY 156 DTKYQSVYVISEE 168  
Db DTKYQSVYVISEE 168

Db 247 DSQEQLVHINSE 259

## RESULT 6

T29311

Hypothetical protein F36D4.3 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C:Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 15-Oct-1999

C:Accession: T29311

R:Pauley, A.; Gattung, S.

submitted to the EMBL Data Library, March 1996

A:Description: The sequence of C. elegans cosmid F36D4.

A:Reference number: Z20603

A:Accession: T29311

A:Status: preliminary; translated from GB/EMBL/DBBJ

A:Molecule type: DNA

A:Residues: 1-925 &lt;PAU&gt;

A:Cross-references: EMBL:U53181; PIDN:AAA93485.1; GSPDB:GN00023; CESP:F36D4.3

A:Experimental source: strain Bristol N2; clone F36D4

C:Genetics:

A:Gene: CESP:F36D4.3

A:Map position: 5

A:Introns: 24/3; 56/2; 103/3; 187/1; 387/2; 429/3; 455/3; 516/1; 555/1; 782/2; 882/3

## Query Match

Best Local Similarity 9.4%; Score 87.5; DB 2; Length 925;

Matches 33; Conservative 17; Mismatches 45; Indels 37; Gaps 4;

QY 7 NCQREKDISVSIIGATGXNTNKKADFXKDXSKNGKQKARYPSVD--YNLVQD---- 60

Db 244 HCQRETERMKAIIEASTLIETL-----DKKTSLKAPESIRVGELEGAYNRLKNDMER 295

QY 61 -----LKGDDTAVRTSHSKRDTKCPSPGSSGRRRPRPHSGXA 98

Db 296 LVSGENGATHSVFERIMEENRLEBEAVELRSMLSHFQKSVAGSSGYRRSPRSDSGH- 354

QY 99 CCGPGSGGGTGW 110

Db 355 CSGADSEDDSSG 366

## RESULT 7

T13475

Hypothetical protein 34F3.1 - fruit fly (Drosophila melanogaster)

C:Species: Drosophila melanogaster

C:Date: 13-Aug-1999 #sequence\_revision 13-Aug-1999 #text\_change 17-Nov-2000

C:Accession: T13475

R:Valenti, P.; Salles, C.; Campbell, L.; Glover, D.

submitted to the EMBL Data Library, April 1999

A:Description: Sequencing the distal X chromosome of Drosophila melanogaster.

A:Reference number: Z17685

A:Accession: T13475

A:Status: preliminary; translated from GB/EMBL/DBBJ

A:Molecule type: DNA

A:Residues: 1-504 &lt;PHI&gt;

A:Cross-references: EMBL:AL031583; NID:el321005; PID:el321015; PIDN:CAA20900.1

C:Genetics:

A:Cross-references: FlyBase:FBgn0025623

A:Note: EG:34F3.1

## Query Match

Best Local Similarity 9.3%; Score 86.5; DB 2; Length 504;

Matches 41; Conservative 16; Mismatches 46; Indels 51; Gaps 10;

QY 49 RYPSVD---YNLVQD-LKGDDTAVRTSHSKRDTKCPSPG-----SSGRRRGRPHS 95

Db 303 RPPSWEAKIYQVANDGLAGAGTGTSTAES---TASQEPDIQDGMGTNLNGRRHG-HGHG 358

QY 96 GXACCGPGSGGGTGW-----VSSWNHCSVSLPKCSHAFIVDFLYPFPFSGEA 141

Db 359 SGTGTGTDGHTLGTSTPTGTPPPRQQQTASGGFCDISVP-----VYATVKGRA 408

QY 142 SE-RRRPDSGCGTSKDTKYQSVYVISEEKDECVI 174

Db 409 SQIRSMPTFG-DSSDDS-----SDGEDHAM 433

## RESULT 8

T14160

Transmembrane receptor protein Robol - rat

C:Species: Rattus norvegicus (Norway rat)

C:Date: 20-Sep-1999 #sequence\_revision 20-Sep-1999 #text\_change 09-Jul-2004

C:Accession: T14160

R:Kidd, T.; Brose, K.; Mitchell, K.J.; Fetter, R.D.; Tessier-Lavigne, M.; Goodman, C.S.;

Cell 92, 205-215, 1998

A:Title: Roundabout controls axon crossing of the CNS midline and defines a novel subfam

A:Reference number: Z17897; MUID:98117249; PMID:9458045

A:Accession: T14160

A:Status: preliminary; translated from GB/EMBL/DBBJ

A:Molecule type: mRNA

A:Residues: 1-1651 &lt;KID&gt;

A:Cross-references: UNIPROT:O55005; EMBL:AF041082; NID:g2811215; PID:g2811216; PIDN:AAC33

C:Function:

A:Description: appears to function as the gatekeeper controlling midline crossing

C:Keywords: transmembrane protein

## Query Match

Best Local Similarity 9.0%; Score 83.5; DB 2; Length 1651;

Matches 29; Conservative 16; Mismatches 40; Indels 33; Gaps 5;

QY 15 SVSIIGATGXNTNKKADFXKDXSKDN----GFKARYPSVDYNLVQ-----DLKGD 64

Db 1075 TTQLIQANLINMNN-----GGGDSSEKHWKPPGQKQEVAPIQYNIMEQNKLKDYRAN 1129

QY 65 DTAVRT-----SHSKRDTKCPSPGSSGRRRGRPHSGKACCGPGSGGTW 109

Db 1130 DTILPTIPNHSYDQNTGGSYNSDRGSTSGQHKKGARTPK-----APQGGGNW 1182

## RESULT 9

T18951

Hypothetical protein C05C12.3 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C:Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 09-Jul-2004

C:Accession: T18951

R:White, S.

submitted to the EMBL Data Library, January 1996

A:Reference number: Z19050

A:Accession: T18951

A:Status: preliminary; translated from GB/EMBL/DBBJ

A:Molecule type: DNA

A:Residues: 1-1707 &lt;WIL&gt;

A:Cross-references: UNIPROT:O17652; EMBL:Z68333; PIDN:CAA92726.1; GSPDB:GN00022; CESP:C05

A:Experimental source: clone C05C12

C:Genetics:

A:Gene: CESP:C05C12.3

A:Map position: 4

A:Introns: 13/3; 82/3; 100/3; 174/3; 203/1; 249/2; 292/1; 358/2; 406/2; 436/2; 477/

542/3; 1595/1; 1647/2; 1673/3; 1695/3

## Query Match

Best Local Similarity 9.0%; Score 83; DB 2; Length 1707;

Matches 32; Conservative 22; Mismatches 49; Indels 54; Gaps 5;

QY 51 PSVDYNLVQDLKGDDTAVRTSHSKRDTKCS----- 81

Db 10 FAHKVAESLRANSVTVEESESERETQTQRRRKORSTSSDKAPLNSAPRHVQKFW 69

QY 82 -----PGSSRRRG--PRPHSGKACCGPGSGGTGWSSWNHCSVSLPKCSHAFIVDFL 133

Db 70 KDLMLHADISGRKGNSTTSHGHA-----FAGSLKGNKWNIECLKMRQCS----- 116

QY 134 YFPFSGEASERKRPDSGCGTSKDTKYQSVYVISEEKD 170

Db 117 YFVPSQRFSE-----CGGCKERSKHTEVLSRSQNK 149





Query Match 8.5%; Score 78.5; DB 2; Length 512;  
Best Local Similarity 26.2%; Pred. No. 7.1;  
Matches 32; Conservative 7; Mismatches 54; Indels 29; Gaps 4;

QY 12 KDTSVSIIGATGIXNTWKADFFXGXDKSSDKNGFQKARYPSVDYNLVDLKGGDTAVRTS 71  
DB ||| ||| : | : | : | : | : | : | : | : | : | : | : | : | : | : | :  
72 KDIRVD--DRVGFQNHNENLSITNADKSSDRNSGKMVSYL-----RTX 113

QY 72 HSKRDTKCQSPGSGRRRRPRPHSGXACCGPGGGGTWGVSSWNHCS-----VSLPKC 124  
DB ||| ||| : | : | : | : | : | : | : | : | : | : | : | : | : | : | :  
114 SSDNDSTISQCSSVHHHERACSSHSGE----DGSFGAAWRQNSLSQGGLVTASPLVLGLPEI 169

QY 125 SH 126  
DB || ||  
170 SH 171

RESULT 14  
T49418  
hypothetical protein BID4.330 [imported] - Neurospora crassa  
C:Species: Neurospora crassa  
C:Date: 02-Jun-2000 #sequence\_revision 02-Jun-2000 #text\_change 09-Jul-2004  
C:Accession: T49418  
R:Schulte, U.; Agn, V.; Hohetsel, J.; Brandt, P.; Fartmann, B.; Holland, R.; Nyakatura,  
submitted to the Protein Sequence Database, May 2000  
A:Reference number: 225022  
A:Accession: T49418  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-538 <SCH>  
A:A:Cross-references: UNIPROT: Q9P649; EMBL: AL355928; GSPDB: GN00116; NCSP: BID4.330  
A:A:Experimental source: BAC clone BID4; strain OR74A  
C:Genetics:  
A:Gene: NCSP:BID4.330  
A:Map position: 6  
A:Introns: 162/2

Query Match 8.4%; Score 77.5; DB 2; Length 538;  
Best Local Similarity 24.0%; Pred. No. 9.3;  
Matches 35; Conservative 18; Mismatches 48; Indels 45; Gaps 9;

QY 46 QKARYPSVDYNLVDLKGGDTAVRTSHSKDTCQSPGSSGRR-----RGPRPHSGX 97  
DB ||| ||| : | : | : | : | : | : | : | : | : | : | : | : | : | : | :  
95 QHAQYQ--HYHAV---TGDNKKATTAKKHGP-EAPGGEGRKFPACPFQOHNPARYTVK 148

QY 98 ACCPGSGGGTGWG-----SSWNHCSVSLPKCSHAFIVDFLYPPFSGEASERK 145  
DB ||||| ||| : | : | : | : | : | : | : | : | : | : | : | : | : | : | :  
149 TCCGPG-----WDVHRVKHHYRRHSLNKTC----PCDYDQFKTD-----DDLKRHQ 192

QY 146 RPDSGGCTSKDTRYQSVYVISBEKDE 171  
DB ||| ||| : | : | : | : | : | : | : | : | : | : | : | : | : | : | :  
193 RAETPCRLRKDNPVE---VITDEQDK 215

RESULT 15  
C96623  
hypothetical protein F23H11.22 [imported] - Arabidopsis thaliana  
C:Species: Arabidopsis thaliana (mouse-ear cress)  
C:Date: 02-Mar-2001 #sequence\_revision 02-Mar-2001 #text\_change 09-Jul-2004  
C:Accession: C96623  
R:Theologas, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,  
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.  
ansen, N.F.; Hughes, B.; Huizar, L.  
Nature 408, 816-820, 2000  
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.  
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziani,  
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.  
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,  
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.  
A:title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.  
A:Reference number: A86141; MUID: I2016719; PMID: 11130712  
A:Accession: C96623  
A:Status: preliminary

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A:Molecule type: DNA
A:Residues: 1-929 <STO>
A:Cross-references: UNIPROT_Q9XIE0; GB:AE005173; NID:G5080823; PIDN:AAD39332.1; GSPDB:GN000001
C:Genetics:
A:Gene: F23H11.22
A:Map position: 1

      Query Match      8.4%; Score 77.5; DB 2; Length 929;
      Best Local Similarity 32.6%; Pred. No. 16;
      Matches 30; Conservative 11; Mismatches 46; Indels 5; Gaps 3;

Qy      36  GDXSSDKNGFGQKARYPSVDYLNVLQDKDDTAVRTSHSKRDTKCGSPGSSGRRGPRPHS 95
      |||:::|||||:::|||||
Db      103  GDKSGD--GFRGTGADQDNDGDDEVDGE--SIEAFSPHVVKQSASSSGGEIRDQNN 159
      |||:::|||||:::|||||

Qy      96  GXACCCGPGSGGTTGVSWNHCSVSLPKCSHA 127
      |||:::|||||
Db      160  GGGGGGGGGGGGGRYYTSS--SASPSRPSSSSA 189
      |||:::|||||

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Search completed: December 2, 2004, 04:02:06  
Job time : 41 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: December 2, 2004, 04:01:28 ; Search time 3243 Seconds  
(without alignments)  
19.244 Million cell updates/sec

Title: US-09-783-931-23

Perfect score: 926

Sequence: 1 TWMNLNQCQREKDISVSIIG.....DTKYGVVVISSEKDCVIA 175

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1582122 seqs, 356623098 residues

Total number of hits satisfying chosen parameters: 1582122

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:\*

- 1: /cgn2\_6/ptodata/1/pubpaa/US07\_PUBCOMB.pap:\*
- 2: /cgn2\_6/ptodata/1/pubpaa/PCT\_NEW\_PUB.pap:\*
- 3: /cgn2\_6/ptodata/1/pubpaa/US06\_NEW\_PUB.pap:\*
- 4: /cgn2\_6/ptodata/1/pubpaa/US06\_PUBCOMB.pap:\*
- 5: /cgn2\_6/ptodata/1/pubpaa/US07\_NEW\_PUB.pap:\*
- 6: /cgn2\_6/ptodata/1/pubpaa/PCTUS\_PUBCOMB.pap:\*
- 7: /cgn2\_6/ptodata/1/pubpaa/US08\_NEW\_PUB.pap:\*
- 8: /cgn2\_6/ptodata/1/pubpaa/US08\_PUBCOMB.pap:\*
- 9: /cgn2\_6/ptodata/1/pubpaa/US09A\_PUBCOMB.pap:\*
- 10: /cgn2\_6/ptodata/1/pubpaa/US09B\_PUBCOMB.pap:\*
- 11: /cgn2\_6/ptodata/1/pubpaa/US09C\_PUBCOMB.pap:\*
- 12: /cgn2\_6/ptodata/1/pubpaa/US09\_NEW\_PUB.pap:\*
- 13: /cgn2\_6/ptodata/1/pubpaa/US10A\_PUBCOMB.pap:\*
- 14: /cgn2\_6/ptodata/1/pubpaa/US10B\_PUBCOMB.pap:\*
- 15: /cgn2\_6/ptodata/1/pubpaa/US10C\_PUBCOMB.pap:\*
- 16: /cgn2\_6/ptodata/1/pubpaa/US10D\_PUBCOMB.pap:\*
- 17: /cgn2\_6/ptodata/1/pubpaa/US10\_NEW\_PUB.pap:\*
- 18: /cgn2\_6/ptodata/1/pubpaa/US11\_NEW\_PUB.pap:\*
- 19: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB.pap:\*
- 20: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	916	98.9	175	9	US-09-908-322-23
2	916	98.9	175	10	US-09-783-931-23
3	631.5	68.2	118	9	US-09-908-322-17
4	631.5	68.2	118	10	US-09-783-931-17
5	527.5	57.0	702	9	US-09-995-593A-4
6	527.5	57.0	723	9	US-09-828-366-21
7	527.5	57.0	723	9	US-09-995-593A-9
8	527.5	57.0	723	14	US-10-028-072-346
9	527.5	57.0	723	14	US-10-140-808-346
10	527.5	57.0	723	14	US-10-121-049-346
11	527.5	57.0	723	14	US-10-123-904-346
12	527.5	57.0	723	14	US-10-140-470-346
13	527.5	57.0	723	14	US-10-175-746-346

14	527.5	57.0	723	14	US-10-176-918-346
15	527.5	57.0	723	14	US-10-176-921-346
16	527.5	57.0	723	14	US-10-137-855-346
17	527.5	57.0	723	14	US-10-140-474-346
18	527.5	57.0	723	14	US-10-142-431-346
19	527.5	57.0	723	14	US-10-143-114-346
20	527.5	57.0	723	14	US-10-140-002-346
21	527.5	57.0	723	14	US-10-142-419-346
22	527.5	57.0	723	14	US-10-241-476-27
23	527.5	57.0	723	14	US-10-123-262-346
24	527.5	57.0	723	14	US-10-142-423-346
25	527.5	57.0	723	14	US-10-121-050-346
26	527.5	57.0	723	14	US-10-141-755-346
27	527.5	57.0	723	14	US-10-143-032-346
28	527.5	57.0	723	14	US-10-123-108-346
29	527.5	57.0	723	14	US-10-123-236-346
30	527.5	57.0	723	14	US-10-123-261-346
31	527.5	57.0	723	14	US-10-140-921-346
32	527.5	57.0	723	14	US-10-140-928-346
33	527.5	57.0	723	14	US-10-121-045-346
34	527.5	57.0	723	14	US-10-123-292-346
35	527.5	57.0	723	14	US-10-123-903-346
36	527.5	57.0	723	14	US-10-124-819-346
37	527.5	57.0	723	14	US-10-124-822-346
38	527.5	57.0	723	14	US-10-140-925-346
39	527.5	57.0	723	14	US-10-160-498-346
40	527.5	57.0	723	14	US-10-124-824-346
41	527.5	57.0	723	14	US-10-127-825A-346
42	527.5	57.0	723	14	US-10-127-829A-346
43	527.5	57.0	723	14	US-10-127-835A-346
44	527.5	57.0	723	14	US-10-127-839A-346
45	527.5	57.0	723	14	US-10-127-901A-346

#### ALIGNMENTS

#### RESULT 1

US-09-908-322-23

; Sequence 23, Application US/09908322

; Patent No. US20020107194A1

; GENERAL INFORMATION:

; APPLICANT: Ish-Horowitz, David

; Henrique, Domingos Manuel Pinto

; Lewis, Julian Hart

; Artavanis-Issakonas, Spyridon

; Gray, Grace

; TITLE OF INVENTION: NUCLEOTIDE AND PROTEIN SEQUENCES OF VERTEBRATE DELTA GENE AND METHODS BASED THEREON

; NUMBER OF SEQUENCES: 94

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Pennie & Edmonds LLP

; STREET: 1155 Avenue of the Americas

; CITY: New York

; STATE: NY

; COUNTRY: USA

; ZIP: 10036/2711

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: DOS

; SOFTWARE: FastSeq Version 2.0

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/908,322

; FILING DATE: 17-Jul-2001

; CLASSIFICATION: <Unknown>

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/981,392

; FILING DATE: 22-DEC-1997

; ATTORNEY/AGENT INFORMATION:

; NAME: Misrock, S Leslie

; REGISTRATION NUMBER: 18,872

; REFERENCE/DOCKET NUMBER: 7326-123

```
;
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-790-9090
; TELEFAX: 212-869-8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 23:
; MOLECULE TYPE: peptide
; SEQUENCE CHARACTERISTICS:
; LENGTH: 175 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 23:
US-09-908-322-23

Query Match          98.9%; Score 916; DB 9; Length 175;
Best Local Similarity 100.0%; Pred. No. 2.6e-86;
Matches 175; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TNNLANCQREKDISVSIIGATGIXNTNKKADFXGDXSDXKNGFQKARYPSVDYNLVQD 60
DB 1 TNNLANCQREKDISVSIIGATGIXNTNKKADFXGDXSDXKNGFQKARYPSVDYNLVQD 60
QY 61 LKGGDTAVRTSHSKRDTKQSPGSSGRRRGRPRPHSGXACCGPGSGGGTGWGVSSWNHCYS 120
DB 61 LKGGDTAVRTSHSKRDTKQSPGSSGRRRGRPRPHSGXACCGPGSGGGTGWGVSSWNHCYS 120
QY 121 LPKCSHAFIVDFLYFPFSGEASERKRPDSCGCTSKDTKYQSVVYVISEEKDECVIA 175
DB 121 LPKCSHAFIVDFLYFPFSGEASERKRPDSCGCTSKDTKYQSVVYVISEEKDECVIA 175

RESULT 2
US-09-783-931-23
; Sequence 23, Application US/09783931
; Publication No. US20030073620A1
; GENERAL INFORMATION:
; APPLICANT: Ish-Horowicz, David
; Henrique, Domingos Manuel Pinto
; Lewis, Julian Hart
; Artavanis-Tsakonas, Spyridon
; Gray, Grace
; TITLE OF INVENTION: ANTIBODIES TO VERTEBRATE DELTA PROTEINS
; NUMBER OF SEQUENCES: 94
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036/2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/783,931
; FILING DATE: 15-Feb-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/981,392
; FILING DATE: 22-DEC-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Antler, Adriane M.
; REGISTRATION NUMBER: 32,605
; REFERENCE/DOCKET NUMBER: 7326-122
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-790-9090
; TELEFAX: 212-869-8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 175 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 23:
US-09-908-322-23

Query Match          98.9%; Score 916; DB 9; Length 175;
Best Local Similarity 100.0%; Pred. No. 2.6e-86;
Matches 175; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TNNLANCQREKDISVSIIGATGIXNTNKKADFXGDXSDXKNGFQKARYPSVDYNLVQD 60
DB 1 TNNLANCQREKDISVSIIGATGIXNTNKKADFXGDXSDXKNGFQKARYPSVDYNLVQD 60
QY 61 LKGGDTAVRTSHSKRDTKQSPGSSGRRRGRPRPHSGXACCGPGSGGGTGWGVSSWNHCYS 120
DB 61 LKGGDTAVRTSHSKRDTKQSPGSSGRRRGRPRPHSGXACCGPGSGGGTGWGVSSWNHCYS 120
QY 121 LPKCSHAFIVDFLYFPFSGEASERKRPDSCGCTSKDTKYQSVVYVISEEKDECVIA 175
DB 121 LPKCSHAFIVDFLYFPFSGEASERKRPDSCGCTSKDTKYQSVVYVISEEKDECVIA 175

RESULT 3
US-09-908-322-17
; Sequence 17, Application US/09908322
; Patent No. US20020107194A1
; GENERAL INFORMATION:
; APPLICANT: Ish-Horowicz, David
; Henrique, Domingos Manuel Pinto
; Lewis, Julian Hart
; Artavanis-Tsakonas, Spyridon
; Gray, Grace
; TITLE OF INVENTION: NUCLEOTIDE AND PROTEIN SEQUENCES OF
; VERTEBRATE DELTA GENE AND METHODS BASED THEREON
; NUMBER OF SEQUENCES: 94
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036/2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/908,322
; FILING DATE: 17-Jul-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/981,392
; FILING DATE: 22-DEC-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Misrock, S Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 7326-123
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-790-9090
; TELEFAX: 212-869-8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 118 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 17:
US-09-783-931-23
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US-09-908-322-17

Query Match 68.2%; Score 631.5; DB 9; Length 118;  
Best Local Similarity 99.2%; Pred. No. 3.8e-57; Indels 1; Gaps 1;  
Matches 118; Conservative 0; Mismatches 0; Indels 1; Gaps 1;  
QY 57 LVQDLKGGDDTAVRTSHSKRDTCQSPGSGRRGPRPHSGXACCPCGSGGGTGWGVSSWNH 116  
DB 1 LVQDLKGGDDTAVRTSHSKRDTCQSPGSGRRGPRPHSGXACCPCGSGGGTGWGVSSW-H 59  
QY 117 CSVSLPKCSHAFIVDFLYPPFSGEASERKRPDSCGTSKDTKYQSVYVISEKDECVIA 175  
DB 60 CSVSLPKCSHAFIVDFLYPPFSGEASERKRPDSCGTSKDTKYQSVYVISEKDECVIA 118

RESULT 4

US-09-783-931-17  
; Sequence 17, Application US/09783931  
; Publication No. US20030073620A1  
; GENERAL INFORMATION:  
; APPLICANT: Ieh-Horowicz, David  
; Henrique, Domingos Manuel Pinto  
; Lewis, Julian Hart  
; Artavanis-Tsakonas, Spyridon  
; Gray, Grace  
; TITLE OF INVENTION: ANTIBODIES TO VERTEBRATE DELTA PROTEINS  
; NUMBER OF SEQUENCES: 94  
; CORRESPONDENCE ADDRESS:  
; ADDRESSER: Pennie & Edmonds LLP  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: NY  
; COUNTRY: USA  
; ZIP: 10036/2711  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/783,931  
; FILING DATE: 15-Feb-2001  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/981,392  
; FILING DATE: 22-DEC-1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Antler, Adriane M.  
; REGISTRATION NUMBER: 32,605  
; REFERENCE/DOCKET NUMBER: 7326-122  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 212-790-9090  
; TELEFAX: 212-869-8864  
; INFORMATION FOR SEQ ID NO: 17:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 118 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: <Unknown>  
; TOPOLOGY: unknown  
; MOLECULE TYPE: peptide  
; SEQUENCE DESCRIPTION: SEQ ID NO: 17:

US-09-783-931-17

Query Match 68.2%; Score 631.5; DB 10; Length 118;  
Best Local Similarity 99.2%; Pred. No. 3.8e-57; Indels 1; Gaps 1;  
Matches 118; Conservative 0; Mismatches 0; Indels 1; Gaps 1;  
QY 57 LVQDLKGGDDTAVRTSHSKRDTCQSPGSGRRGPRPHSGXACCPCGSGGGTGWGVSSWNH 116  
DB 1 LVQDLKGGDDTAVRTSHSKRDTCQSPGSGRRGPRPHSGXACCPCGSGGGTGWGVSSW-H 59

QY 117 CSVSLPKCSHAFIVDFLYPPFSGEASERKRPDSCGTSKDTKYQSVYVISEKDECVIA 175  
DB 60 CSVSLPKCSHAFIVDFLYPPFSGEASERKRPDSCGTSKDTKYQSVYVISEKDECVIA 118

RESULT 5

US-09-995-593A-4  
; Sequence 4, Application US/09995593A  
; Patent No. US20020128197A1  
; GENERAL INFORMATION:  
; APPLICANT: SAKANO, SEIJI  
; APPLICANT: ITOH, AKIRA  
; TITLE OF INVENTION: DIFFERENTIATION-SUPPRESSIVE POLYPEPTIDE  
; FILE REFERENCE: KP8447DIV  
; CURRENT APPLICATION NUMBER: US/09/995,593A  
; CURRENT FILING DATE: 2002-02-28  
; PRIOR APPLICATION NUMBER: 09/068,740  
; PRIOR FILING DATE: 1998-06-18  
; PRIOR APPLICATION NUMBER: JP 7-299611  
; PRIOR FILING DATE: 1995-11-17  
; PRIOR APPLICATION NUMBER: JP 7-311811  
; PRIOR FILING DATE: 1995-11-30  
; PRIOR APPLICATION NUMBER: PCT/JP96/03356  
; PRIOR FILING DATE: 1996-11-15  
; NUMBER OF SEQ ID NOS: 48  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 4  
; LENGTH: 702  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-995-593A-4

Query Match 57.0%; Score 527.5; DB 9; Length 702;  
Best Local Similarity 64.8%; Pred. No. 1.8e-45; Indels 45; Gaps 4;  
Matches 114; Conservative 4; Mismatches 13; Indels 45; Gaps 4;  
QY 1 TMNNLANCQREKDISVSIIGATGIXNTNKADFXGXGDSXSSDKNGFQKARYPSVDYNLVQD 60  
DB 568 TMNNLANCQREKDISVSIIGATGIXNTNKADFXGXGDSXSSDKNGFQKARYPSVDYNLVQD 625  
QY 61 LKGGDTAVRTSHSKRDTCQSPGSGRRRG-PRPHSGXACCPCGSGGGTGWGVSSWNHCSV 119  
DB 626 LKGGDTAVRTSHSKRDTCQSPGSGRRRG-PRPHSGXACCPCGSGGGTGWGVSSWNHCSV 662  
QY 120 SLPKCSHAFIVDFLYPPFSGEASERKRPDSCGTSKDTKYQSVYVISEKDECVIA 175  
DB 663 -----GEASERKRPDSCGTSKDTKYQSVYVISEKDECVIA 699

RESULT 6

US-09-828-366-21  
; Sequence 21, Application US/09828366  
; Patent No. US20020010137A1  
; GENERAL INFORMATION:  
; APPLICANT: Genentech, Inc.  
; APPLICANT: Ashkenazi, Avi  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Klein, Robert D.  
; APPLICANT: Napier, Mary  
; APPLICANT: Wood, William I.  
; APPLICANT: Yuan, Jean  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITING NEOPLASTIC  
; FILE REFERENCE: P1694RIC1  
; CURRENT APPLICATION NUMBER: US/09/828,366  
; CURRENT FILING DATE: 2001-04-05  
; Prior filing data removed - refer to PALM or file wrapper  
; NUMBER OF SEQ ID NOS: 29  
; SEQ ID NO 21  
; LENGTH: 723  
; TYPE: PRT  
; ORGANISM: Homo sapien

US-09-828-366-21

Query Match 57.0%; Score 527.5; DB 9; Length 723;  
Best Local Similarity 64.8%; Pred. No. 1.8e-45;  
Matches 114; Conservative 4; Mismatches 13; Indels 45; Gaps 4;  
  
QY 1 TMNLANCQREKDISVSIIGATGIXNTNKKADFPXGDXSDXNGFQKARYPSVDYNLVQD 60  
Db 589 TMNLANCQREKDISVSIIGATGIXNTNKKADFPXGDXSDXNGFQKARYPSVDYNLVQD 646  
QY 61 LKGGDTAVRTSHSKRDTKCPQSSGRRRG-PRPHSGXACCGPGSGGTWGVSSWNHCSV 119  
Db 647 LKGGDTAVRDADHAKRDTKCPQSSGEEKGTPTLRG----- 683  
  
QY 120 SLPKCSHAFTVDFLYPFGSEASERKPDGCGTSTKDTKYQSVYVISEEKDECVIA 175  
Db 684 -----GEASERKPDGCGTSTKDTKYQSVYVISEEKDECVIA 720

## RESULT 7

US-09-995-593A-9  
; Sequence 9, Application US/09995593A  
; Patent No. US20020128197A1  
; GENERAL INFORMATION:  
; APPLICANT: SAKANO, SEIJI  
; APPLICANT: ITOH, AKIRA  
; TITLE OF INVENTION: DIFFERENTIATION-SUPPRESSIVE POLYPEPTIDE  
; FILE REFERENCE: KP8447DIV  
; CURRENT APPLICATION NUMBER: US/09/995,593A  
; CURRENT FILING DATE: 2002-02-28  
; PRIOR APPLICATION NUMBER: 09/068,740  
; PRIOR FILING DATE: 1998-06-18  
; PRIOR APPLICATION NUMBER: JP 7-299611  
; PRIOR FILING DATE: 1995-11-17  
; PRIOR APPLICATION NUMBER: JP 7-311811  
; PRIOR FILING DATE: 1995-11-30  
; PRIOR APPLICATION NUMBER: PCT/JP96/03356  
; PRIOR FILING DATE: 1996-11-15  
; NUMBER OF SEQ ID NOS: 48  
; SOFTWARE: Patent In Ver. 2.1  
; SEQ ID NO 9  
; LENGTH: 723  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-995-593A-9

Query Match 57.0%; Score 527.5; DB 9; Length 723;  
Best Local Similarity 64.8%; Pred. No. 1.8e-45;  
Matches 114; Conservative 4; Mismatches 13; Indels 45; Gaps 4;  
  
QY 1 TMNLANCQREKDISVSIIGATGIXNTNKKADFPXGDXSDXNGFQKARYPSVDYNLVQD 60  
Db 589 TMNLANCQREKDISVSIIGATGIXNTNKKADFPXGDXSDXNGFQKARYPSVDYNLVQD 646  
QY 61 LKGGDTAVRTSHSKRDTKCPQSSGRRRG-PRPHSGXACCGPGSGGTWGVSSWNHCSV 119  
Db 647 LKGGDTAVRDADHAKRDTKCPQSSGEEKGTPTLRG----- 683  
  
QY 120 SLPKCSHAFTVDFLYPFGSEASERKPDGCGTSTKDTKYQSVYVISEEKDECVIA 175  
Db 684 -----GEASERKPDGCGTSTKDTKYQSVYVISEEKDECVIA 720

## RESULT 8

US-10-028-072-346  
; Sequence 346, Application US/10028072  
; Publication No. US20030004311A1  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Beresini, Maureen  
; APPLICANT: DeForge, Laura  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Filvaroff, Ellen

; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Goddowski, Paul J.  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Sherwood, Steven  
; APPLICANT: Smith, Victoria  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Watanabe, Colin K  
; APPLICANT: Wood, William  
; APPLICANT: Zhang  
; TITLE OF INVENTION:  
; FILE REFERENCE:  
; CURRENT APPLICATION NUMBER: US/10/028,072  
; CURRENT FILING DATE: 2001-12-19  
; PRIOR APPLICATION NUMBER: 60/049911  
; PRIOR FILING DATE: 1997-06-18  
; PRIOR APPLICATION NUMBER: 60/056974  
; PRIOR FILING DATE: 1997-08-26  
; PRIOR APPLICATION NUMBER: 60/059113  
; PRIOR FILING DATE: 1997-09-17  
; PRIOR APPLICATION NUMBER: 60/059115  
; PRIOR FILING DATE: 1997-09-17  
; PRIOR APPLICATION NUMBER: 60/059117  
; PRIOR FILING DATE: 1997-09-17  
; PRIOR APPLICATION NUMBER: 60/059122  
; PRIOR FILING DATE: 1997-09-17  
; PRIOR APPLICATION NUMBER: 60/059184  
; PRIOR FILING DATE: 1997-09-17  
; PRIOR APPLICATION NUMBER: 60/059263  
; PRIOR FILING DATE: 1997-09-18  
; PRIOR APPLICATION NUMBER: 60/059352  
; PRIOR FILING DATE: 1997-09-19  
; PRIOR APPLICATION NUMBER: 60/059588  
; PRIOR FILING DATE: 1997-09-19  
; PRIOR APPLICATION NUMBER: 60/059836  
; PRIOR FILING DATE: 1997-09-24  
; PRIOR APPLICATION NUMBER: 60/062250  
; PRIOR FILING DATE: 1997-10-17  
; PRIOR APPLICATION NUMBER: 60/062285  
; PRIOR FILING DATE: 1997-10-17  
; PRIOR APPLICATION NUMBER: 60/062287  
; PRIOR FILING DATE: 1997-10-17  
; PRIOR APPLICATION NUMBER: 60/062814  
; PRIOR FILING DATE: 1997-10-24  
; PRIOR APPLICATION NUMBER: 60/062816  
; PRIOR FILING DATE: 1997-10-24  
; PRIOR APPLICATION NUMBER: 60/063045  
; PRIOR FILING DATE: 1997-10-24  
; PRIOR APPLICATION NUMBER: 60/063082  
; PRIOR FILING DATE: 1997-10-31  
; PRIOR APPLICATION NUMBER: 60/063127  
; PRIOR FILING DATE: 1997-10-24  
; PRIOR APPLICATION NUMBER: 60/063327  
; PRIOR FILING DATE: 1997-10-27  
; PRIOR APPLICATION NUMBER: 60/063329  
; PRIOR FILING DATE: 1997-10-27  
; PRIOR APPLICATION NUMBER: 60/063550  
; PRIOR FILING DATE: 1997-10-28  
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; PRIOR FILING DATE: 1997-10-29  
; PRIOR APPLICATION NUMBER: 60/063735  
; PRIOR FILING DATE: 1997-10-29  
; PRIOR APPLICATION NUMBER: 60/063738  
; PRIOR FILING DATE: 1997-10-29  
; PRIOR APPLICATION NUMBER: 60/063755  
; PRIOR FILING DATE: 1997-10-17  
; PRIOR APPLICATION NUMBER: 60/064248

; PRIOR FILING DATE: 1997-11-03  
 ; PRIOR APPLICATION NUMBER: 60/064809  
 ; PRIOR FILING DATE: 1997-11-07  
 ; PRIOR APPLICATION NUMBER: 60/065186  
 ; PRIOR FILING DATE: 1997-11-12  
 ; PRIOR APPLICATION NUMBER: 60/065846  
 ; PRIOR FILING DATE: 1997-11-17  
 ; PRIOR APPLICATION NUMBER: 60/066364  
 ; PRIOR FILING DATE: 1997-11-21  
 ; PRIOR APPLICATION NUMBER: 60/066453  
 ; PRIOR FILING DATE: 1997-11-24  
 ; PRIOR APPLICATION NUMBER: 60/066511  
 ; PRIOR FILING DATE: 1997-11-24  
 ; PRIOR APPLICATION NUMBER: 60/066770  
 ; PRIOR FILING DATE: 1997-11-24  
 ; PRIOR APPLICATION NUMBER: 60/069212  
 ; PRIOR FILING DATE: 1997-12-11  
 ; PRIOR APPLICATION NUMBER: 60/069278  
 ; PRIOR FILING DATE: 1997-12-11  
 ; PRIOR APPLICATION NUMBER: 60/069334  
 ; PRIOR FILING DATE: 1997-12-11  
 ; PRIOR APPLICATION NUMBER: 60/069694  
 ; PRIOR FILING DATE: 1997-12-16  
 ; PRIOR APPLICATION NUMBER: 60/072320  
 ; PRIOR FILING DATE: 1998-01-23  
 ; PRIOR APPLICATION NUMBER: 60/073612  
 ; PRIOR FILING DATE: 1998-02-04  
 ; PRIOR APPLICATION NUMBER: 60/074086  
 ; PRIOR FILING DATE: 1998-02-09  
 ; PRIOR APPLICATION NUMBER: 60/074092  
 ; PRIOR FILING DATE: 1998-02-09  
 ; PRIOR APPLICATION NUMBER: 60/077791  
 ; PRIOR FILING DATE: 1998-03-12  
 ; PRIOR APPLICATION NUMBER: 60/078910  
 ; PRIOR FILING DATE: 1998-03-20  
 ; PRIOR APPLICATION NUMBER: 60/079294  
 ; PRIOR FILING DATE: 1998-03-25  
 ; PRIOR APPLICATION NUMBER: 60/079663  
 ; PRIOR FILING DATE: 1998-02-27  
 ; PRIOR APPLICATION NUMBER: 60/079728  
 ; PRIOR FILING DATE: 1998-03-27  
 ; PRIOR APPLICATION NUMBER: 60/080165  
 ; PRIOR FILING DATE: 1998-03-31  
 ; PRIOR APPLICATION NUMBER: 60/081203  
 ; PRIOR FILING DATE: 1998-04-09  
 ; PRIOR APPLICATION NUMBER: 60/081229  
 ; PRIOR FILING DATE: 1998-04-09  
 ; PRIOR APPLICATION NUMBER: 60/081695  
 ; PRIOR FILING DATE: 1998-04-14  
 ; PRIOR APPLICATION NUMBER: 60/081817  
 ; PRIOR FILING DATE: 1998-04-15  
 ; PRIOR APPLICATION NUMBER: 60/081818  
 ; PRIOR FILING DATE: 1998-04-15  
 ; PRIOR APPLICATION NUMBER: 60/082999  
 ; PRIOR FILING DATE: 1998-04-24  
 ; PRIOR APPLICATION NUMBER: 60/083322  
 ; PRIOR FILING DATE: 1998-04-28  
 ; PRIOR APPLICATION NUMBER: 60/083545  
 ; PRIOR FILING DATE: 1998-04-29  
 ; PRIOR APPLICATION NUMBER: 60/084600  
 ; PRIOR FILING DATE: 1998-05-07  
 ; PRIOR APPLICATION NUMBER: 60/084627  
 ; PRIOR FILING DATE: 1998-05-07  
 ; PRIOR APPLICATION NUMBER: 60/084637  
 ; PRIOR FILING DATE: 1998-05-07  
 ; PRIOR APPLICATION NUMBER: 60/085149  
 ; PRIOR FILING DATE: 1998-05-12  
 ; PRIOR APPLICATION NUMBER: 60/085323  
 ; PRIOR FILING DATE: 1998-05-13  
 ; PRIOR APPLICATION NUMBER: 60/085338  
 ; PRIOR FILING DATE: 1998-05-13  
 ; PRIOR APPLICATION NUMBER: 60/085339  
 ; PRIOR FILING DATE: 1998-05-13

; PRIOR APPLICATION NUMBER: 60/085579  
 ; PRIOR FILING DATE: 1998-05-15  
 ; PRIOR APPLICATION NUMBER: 60/085697  
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 ; PRIOR APPLICATION NUMBER: 60/086414  
 ; PRIOR FILING DATE: 1998-05-22  
 ; PRIOR APPLICATION NUMBER: 60/086430  
 ; PRIOR FILING DATE: 1998-05-22  
 ; PRIOR APPLICATION NUMBER: 60/087106  
 ; PRIOR FILING DATE: 1998-05-28  
 ; PRIOR APPLICATION NUMBER: 60/088026  
 ; PRIOR FILING DATE: 1998-06-04  
 ; PRIOR APPLICATION NUMBER: 60/088730  
 ; PRIOR FILING DATE: 1998-06-10  
 ; PRIOR APPLICATION NUMBER: 60/088741  
 ; PRIOR FILING DATE: 1998-06-10  
 ; PRIOR APPLICATION NUMBER: 60/088810  
 ; PRIOR FILING DATE: 1998-06-10  
 ; PRIOR APPLICATION NUMBER: 60/088858  
 ; PRIOR FILING DATE: 1998-06-11  
 ; PRIOR APPLICATION NUMBER: 60/089532  
 ; PRIOR FILING DATE: 1998-06-17  
 ; PRIOR APPLICATION NUMBER: 60/089599  
 ; PRIOR FILING DATE: 1998-06-17  
 ; PRIOR APPLICATION NUMBER: 60/089907  
 ; PRIOR FILING DATE: 1998-06-18  
 ; PRIOR APPLICATION NUMBER: 60/089947  
 ; PRIOR FILING DATE: 1998-06-19  
 ; PRIOR APPLICATION NUMBER: 60/090349  
 ; PRIOR FILING DATE: 1998-06-23  
 ; PRIOR APPLICATION NUMBER: 60/090429  
 ; PRIOR FILING DATE: 1998-06-24  
 ; PRIOR APPLICATION NUMBER: 60/090445  
 ; PRIOR FILING DATE: 1998-06-24  
 ; PRIOR APPLICATION NUMBER: 60/090538  
 ; PRIOR FILING DATE: 1998-06-24  
 ; PRIOR APPLICATION NUMBER: 60/090863  
 ; PRIOR FILING DATE: 1998-06-26  
 ; PRIOR APPLICATION NUMBER: 60/091360  
 ; PRIOR FILING DATE: 1998-07-01  
 ; PRIOR APPLICATION NUMBER: 60/091519  
 ; PRIOR FILING DATE: 1998-07-02  
 ; PRIOR APPLICATION NUMBER: 60/091982  
 ; PRIOR FILING DATE: 1998-07-07

Query Match 57.0%; Score 527.5; DB 14; Length 723;  
 Best Local Similarity 64.8%; Pred. No. 1.8e-45;  
 Matches 114; Conservative 4; Mismatches 13; Indels 45; Gaps 4;  
 QY 1 TNNLANCOREKDISVSIIGATGIXNTNKKADFXKXGDSXNDKNGKQKARYPSVDYNLVQD 60  
 DB 589 TNNLANCOREKDISVSIIGATGIXNTNKKADFXKXGDSXNDKNGKQKARYPSVDYNLVQD 646  
 QY 61 LKGGDTAVRTSHSKEDTKCQSPGSSGRRRG-PRPHSGXACCGPGSGGTWGVSSNNHCSV 119  
 DB 647 LKGGDTAVRDAHSKRDKTKCQPGSSGEEKGTPTTURG-----683  
 QY 120 SLPKCSHAFIVDFLYFPFSGEASERKRPDSGSGTSKDTKYQSVYVISEKDECVIA 175  
 DB 684 -----GEASERKRPDSGSGTSKDTKYQSVYVISEKDECVIA 720

RESULT 9  
 US-10-140-808-346  
 ; Sequence 346, Application US/10140808  
 ; Publication No. US20030017563A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Baker, Kevin P.  
 ; APPLICANT: Beresini, Maureen  
 ; APPLICANT: DeForge, Laura  
 ; APPLICANT: Desnoyers, Luc

```
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C182
; CURRENT APPLICATION NUMBER: US/10/140,808
; PRIOR APPLICATION DATE: 2002-05-07
; PRIOR APPLICATION REMOVED - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 346
; LENGTH: 723
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-140-808-346

Query Match      57.0%; Score 527.5; DB 14; Length 723;
Best Local Similarity 64.8%; Pred. No. 1.8e-45;
Matches 114; Conservative 4; Mismatches 13; Indels 45; Gaps 4;

QY 1 TMNNLANCOREKDISVSIIGATGIXNTNKKADFPXGDXSSDKNGFQKARYPSVDYNLVQD 60
Db 589 TMNNLANCOREKDISVSIIGATGIXNTNKKADFPXGDXSSDKNGFQKARYPSVDYNLVQD 646

QY 61 LKGGDTAVRTSHSKRDTKQSPGSSGRRRG-PRPHSGXACCGPGSGGTWGVSSMNHCSV 119
Db 647 LKGGDTAVRDAHSAKRDTCQPOGSGGEGKGTPTTLRG-----683

QY 120 SLPKCSHAFIVDFLYPPFSGEASERKRPDSCGTSKDTKYQSVYVISEBKDECVIA 175
Db 684 -----GEASERKRPDSCGTSKDTKYQSVYVISEBKDECVIA 720

RESULT 10
US-10-121-049-346
; Sequence 346, Application US/10121049
; Publication No. US2003002239A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C17
; CURRENT APPLICATION NUMBER: US/10/121,049
; PRIOR APPLICATION REMOVED - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 346
; LENGTH: 723
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-121-049-346

Query Match      57.0%; Score 527.5; DB 14; Length 723;
Best Local Similarity 64.8%; Pred. No. 1.8e-45;
Matches 114; Conservative 4; Mismatches 13; Indels 45; Gaps 4;

QY 1 TMNNLANCOREKDISVSIIGATGIXNTNKKADFPXGDXSSDKNGFQKARYPSVDYNLVQD 60
Db 589 TMNNLANCOREKDISVSIIGATGIXNTNKKADFPXGDXSSDKNGFQKARYPSVDYNLVQD 646

QY 61 LKGGDTAVRTSHSKRDTKQSPGSSGRRRG-PRPHSGXACCGPGSGGTWGVSSMNHCSV 119
Db 647 LKGGDTAVRDAHSAKRDTCQPOGSGGEGKGTPTTLRG-----683

QY 120 SLPKCSHAFIVDFLYPPFSGEASERKRPDSCGTSKDTKYQSVYVISEBKDECVIA 175
Db 684 -----GEASERKRPDSCGTSKDTKYQSVYVISEBKDECVIA 720

RESULT 11
US-10-123-904-346
; Sequence 346, Application US/10123904
; Publication No. US20030022328A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C54
; CURRENT APPLICATION NUMBER: US/10/123,904
; PRIOR APPLICATION REMOVED - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 346
; LENGTH: 723
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-123-904-346

Query Match      57.0%; Score 527.5; DB 14; Length 723;
Best Local Similarity 64.8%; Pred. No. 1.8e-45;
Matches 114; Conservative 4; Mismatches 13; Indels 45; Gaps 4;

QY 1 TMNNLANCOREKDISVSIIGATGIXNTNKKADFPXGDXSSDKNGFQKARYPSVDYNLVQD 60
Db 589 TMNNLANCOREKDISVSIIGATGIXNTNKKADFPXGDXSSDKNGFQKARYPSVDYNLVQD 646

QY 61 LKGGDTAVRTSHSKRDTKQSPGSSGRRRG-PRPHSGXACCGPGSGGTWGVSSMNHCSV 119
Db 647 LKGGDTAVRDAHSAKRDTCQPOGSGGEGKGTPTTLRG-----683

QY 120 SLPKCSHAFIVDFLYPPFSGEASERKRPDSCGTSKDTKYQSVYVISEBKDECVIA 175
Db 684 -----GEASERKRPDSCGTSKDTKYQSVYVISEBKDECVIA 720
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; LENGTH: 723
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-121-049-346

Query Match      57.0%; Score 527.5; DB 14; Length 723;
Best Local Similarity 64.8%; Pred. No. 1.8e-45;
Matches 114; Conservative 4; Mismatches 13; Indels 45; Gaps 4;

QY 1 TMNNLANCOREKDISVSIIGATGIXNTNKKADFPXGDXSSDKNGFQKARYPSVDYNLVQD 60
Db 589 TMNNLANCOREKDISVSIIGATGIXNTNKKADFPXGDXSSDKNGFQKARYPSVDYNLVQD 646

QY 61 LKGGDTAVRTSHSKRDTKQSPGSSGRRRG-PRPHSGXACCGPGSGGTWGVSSMNHCSV 119
Db 647 LKGGDTAVRDAHSAKRDTCQPOGSGGEGKGTPTTLRG-----683

QY 120 SLPKCSHAFIVDFLYPPFSGEASERKRPDSCGTSKDTKYQSVYVISEBKDECVIA 175
Db 684 -----GEASERKRPDSCGTSKDTKYQSVYVISEBKDECVIA 720

RESULT 11
US-10-123-904-346
; Sequence 346, Application US/10123904
; Publication No. US20030022328A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C54
; CURRENT APPLICATION NUMBER: US/10/123,904
; PRIOR APPLICATION REMOVED - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 346
; LENGTH: 723
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-123-904-346

Query Match      57.0%; Score 527.5; DB 14; Length 723;
Best Local Similarity 64.8%; Pred. No. 1.8e-45;
Matches 114; Conservative 4; Mismatches 13; Indels 45; Gaps 4;

QY 1 TMNNLANCOREKDISVSIIGATGIXNTNKKADFPXGDXSSDKNGFQKARYPSVDYNLVQD 60
Db 589 TMNNLANCOREKDISVSIIGATGIXNTNKKADFPXGDXSSDKNGFQKARYPSVDYNLVQD 646

QY 61 LKGGDTAVRTSHSKRDTKQSPGSSGRRRG-PRPHSGXACCGPGSGGTWGVSSMNHCSV 119
Db 647 LKGGDTAVRDAHSAKRDTCQPOGSGGEGKGTPTTLRG-----683

QY 120 SLPKCSHAFIVDFLYPPFSGEASERKRPDSCGTSKDTKYQSVYVISEBKDECVIA 175
Db 684 -----GEASERKRPDSCGTSKDTKYQSVYVISEBKDECVIA 720
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RESULT 12
US-10-140-470-346
; Sequence 346, Application US/10140470
; Publication No. US2003002231A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C160
; CURRENT APPLICATION NUMBER: US/10/140,470
; CURRENT FILING DATE: 2002-05-06
; Prior Application removed - See Palm or File Wrapper
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 346
; LENGTH: 723
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-140-470-346

Query Match 57.0%; Score 527.5; DB 14; Length 723;
Best Local Similarity 64.8%; Pred. No. 1.8e-45;
Matches 114; Conservative 4; Mismatches 13; Indels 45; Gaps 4;

QY 1 TNNLANCOREKDISVSIIGATGIXNTNKKADPFXKXGDSKXNGFQKARYPSVDYNLVQD 60
Db 589 TNNLANCOREKDISVSIIGATGIXNTNKKADPFXKXGDSKXNGFQKARYPSVDYNLVQD 646
QY 61 LKGGDTAVRTSHKRDTCQSPGSSGRRRG-PRPHSGXACCGPGSGGTWGVSSMNHCSV 119
Db 647 LKGGDTAVRDAHSKRDTCQSPGSSGEEKGTPPTLRG----- 683
QY 120 SLPKCSHAFIVDFLYPPFSGEASERKRPDSGCGSTSKDTKYQSVYVISEKDECVIA 175
Db 684 -----GEASERKRPDSGCGSTSKDTKYQSVYVISEKDECVIA 720

RESULT 14
US-10-176-918-346
; Sequence 346, Application US/10176918
; Publication No. US2003002275A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C382
; CURRENT APPLICATION NUMBER: US/10/176,918
; CURRENT FILING DATE: 2002-06-20
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 346
; LENGTH: 723
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-176-918-346

Query Match 57.0%; Score 527.5; DB 14; Length 723;
Best Local Similarity 64.8%; Pred. No. 1.8e-45;
Matches 114; Conservative 4; Mismatches 13; Indels 45; Gaps 4;

QY 1 TNNLANCOREKDISVSIIGATGIXNTNKKADPFXKXGDSKXNGFQKARYPSVDYNLVQD 60
Db 589 TNNLANCOREKDISVSIIGATGIXNTNKKADPFXKXGDSKXNGFQKARYPSVDYNLVQD 646
QY 61 LKGGDTAVRTSHKRDTCQSPGSSGRRRG-PRPHSGXACCGPGSGGTWGVSSMNHCSV 119
Db 647 LKGGDTAVRDAHSKRDTCQSPGSSGEEKGTPPTLRG----- 683
QY 120 SLPKCSHAFIVDFLYPPFSGEASERKRPDSGCGSTSKDTKYQSVYVISEKDECVIA 175
Db 684 -----GEASERKRPDSGCGSTSKDTKYQSVYVISEKDECVIA 720

RESULT 13
US-10-175-746-346
; Sequence 346, Application US/10175746
; Publication No. US2003002270A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
```

Db 589 TMNLANCOREKDISVSIIGATQIKNTNKKADF-HGDHSADKNGF-KARYPAVDYNLVQD 646  
Qy 61 LKGGDTAVRTSHSKRDTKQSPGSSGRRRG-PRPHSGXACCGPGSGGTGWGVSSWNHCSV 119  
Db 647 LKGGDTAVRDAHSKRDTKQPOGSSGEEKGTPTLRG----- 683  
Qy 120 SLPKCSHAFIVDFLYPFPGSEASERKRPDSCGCTSKDTKYQSVYVISEEKDECVIA 175  
Db 684 -----GEASERKRPDSCGCTSKDTKYQSVYVISEEKDECVIA 720

RESULT 15  
US-10-176-921-346  
; Sequence 346 Application US/10176921  
; Publication No. US2003002726A1  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Beresini, Maureen  
; APPLICANT: DeForge, Laura  
; APPLICANT: Deenoyera, Luc  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Sherwood, Steven  
; APPLICANT: Smith, Victoria  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Watanabe, Colin K  
; APPLICANT: Wood, William  
; APPLICANT: Zhang, Zemin  
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
; FILE REFERENCE: P330R1C288  
; CURRENT APPLICATION NUMBER: US/10/176,921  
; CURRENT FILING DATE: 2002-06-20  
; Prior Application removed - See File Wrapper or Palm  
; NUMBER OF SEQ ID NOS: 550  
; SEQ ID NO 346  
; LENGTH: 723  
; TYPE: PRT  
; ORGANISM: Homo Sapien  
US-10-176-921-346

Query Match 57.0%; Score 527.5; DB 14; Length 723;  
Best Local Similarity 64.8%; Pred. No. 1.8e-45;  
Matches 114; Conservative 4; Mismatches 13; Indels 45; Gaps 4;  
Qy 1 TMNLANCOREKDISVSIIGATQIKNTNKKADFXXGDXSDKNGFQKARYPSVDYNLVQD 60  
Db 589 TMNLANCOREKDISVSIIGATQIKNTNKKADF-HGDHSADKNGF-KARYPAVDYNLVQD 646  
Qy 61 LKGGDTAVRTSHSKRDTKQSPGSSGRRRG-PRPHSGXACCGPGSGGTGWGVSSWNHCSV 119  
Db 647 LKGGDTAVRDAHSKRDTKQPOGSSGEEKGTPTLRG----- 683  
Qy 120 SLPKCSHAFIVDFLYPFPGSEASERKRPDSCGCTSKDTKYQSVYVISEEKDECVIA 175  
Db 684 -----GEASERKRPDSCGCTSKDTKYQSVYVISEEKDECVIA 720

Search completed: December 2, 2004, 05:08:08  
Job time : 3252 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 2, 2004, 03:51:27 ; Search time 153 Seconds  
(without alignments)  
410.311 Million cell updates/sec

Title: US-09-783-931-23  
Perfect score: 926

Sequence: 1 TNNLANQREKDISVSIIG.....DTKYQSVYVISEKDECVIA 175

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A\_Geneseq\_23Sep04:\*

- 1: Geneseq1980s:\*
- 2: Geneseq1990s:\*
- 3: Geneseq2000s:\*
- 4: Geneseq2001s:\*
- 5: Geneseq2002s:\*
- 6: Geneseq2003as:\*
- 7: Geneseq2003bs:\*
- 8: Geneseq2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	908	98.1	175	2 AAW11724	AAW11724 H-Delta-1
2	678.5	73.3	175	2 AAW11721	AAW11721 H-Delta-1
3	527.5	57.0	702	2 AAW18349	AAW18349 Prolifera
4	527.5	57.0	702	2 AAW75495	AAW75495 Truncated
5	527.5	57.0	723	2 AAW18353	AAW18353 Prolifera
6	527.5	57.0	723	2 AAW75492	AAW75492 Human del
7	527.5	57.0	723	2 AAW94498	AAW94498 Human del
8	527.5	57.0	723	3 AAY833227	AAY833227 PRO172 po
9	527.5	57.0	723	3 AAB333422	AAB333422 Human PRO
10	527.5	57.0	723	3 AAB24388	AAB24388 Human PRO
11	527.5	57.0	723	3 AAY79032	AAY79032 Human del
12	527.5	57.0	723	3 AAB00172	AAB00172 PRO172 po
13	527.5	57.0	723	3 AAW12344	AAW12344 Human PRO
14	527.5	57.0	723	4 AAB53064	AAB53064 Human ang
15	527.5	57.0	723	6 ABO17788	ABO17788 Novel hum
16	527.5	57.0	723	6 ABO81042	ABO81042 Human PRO
17	527.5	57.0	723	6 ABP97824	ABP97824 Amino aci
18	527.5	57.0	723	6 ABU66742	ABU66742 Human PRO
19	527.5	57.0	723	6 ABU55879	ABU55879 Human not
20	527.5	57.0	723	6 AAE34035	AAE34035 Human not
21	527.5	57.0	723	6 ABUS9823	ABUS9823 Novel sec
22	527.5	57.0	723	6 ABO25013	ABO25013 Human sec
23	527.5	57.0	723	6 ABP72566	ABP72566 Human Not
24	527.5	57.0	723	6 ABU67018	ABU67018 Human sec
25	527.5	57.0	723	6 ADA45865	ADA45865 Novel hum

## ALIGNMENTS

## RESULT 1

## AAW11724

ID AAW11724 standard; protein; 175 AA.

XX AAW11724;

XX AC AAW11724;

XX DT 28-APR-1997 (first entry)

XX DE H-Delta-1 polypeptide predicted sequence.

XX H-Delta-1; cell proliferation; nervous system disorder;

KW tissue regeneration; Notch; cervix cancer; breast cancer; lung cancer;

KW colon cancer; melanoma; seminoma; neurogenesis; therapy.

XX OS Homo sapiens.

XX PH Key Location/Qualifiers

FT Misc-difference 25 /note= "undetermined amino acid residue"

FT Misc-difference 34 /note= "undetermined amino acid residue"

FT Misc-difference 35 /note= "undetermined amino acid residue"

FT Misc-difference 38 /note= "undetermined amino acid residue"

FT Misc-difference 97 /note= "undetermined amino acid residue"

FT Misc-difference 97 /note= "undetermined amino acid residue"

FT Misc-difference 97 /note= "undetermined amino acid residue"

FT Misc-difference 97 /note= "undetermined amino acid residue"

FT Misc-difference 97 /note= "undetermined amino acid residue"

FT Misc-difference 97 /note= "undetermined amino acid residue"

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FT Misc-difference 97 /note= "undetermined amino acid residue"

FT Misc-difference 97 /note= "undetermined amino acid residue"

FT Misc-difference 97 /note= "undetermined amino acid residue"

FT Misc-difference 97 /note= "undetermined amino acid residue"

FT Misc-difference 97 /note= "undetermined amino acid residue"

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PS Claim 41; Fig 11; 135pp; English.
XX
CC The amino acid sequence (AAW11724) of H-Delta-1 was predicted by
CC alignment of polypeptides (AAW11721-23) corresponding to the 3 reading
CC frames of an isolated H-Delta-1 gene sequence (AAT58900) with that of
CC chick C-Delta-1 (AAW58897). Because of sequencing errors in the gene
CC sequence, the homology was obtd. by switching amongst the 3 open reading
CC frames to identify homologous regions. H-Delta-1 polypeptide sequences
CC (AAW11725-38) were also deduced from a contig sequence (AAT59454). H-
CC Delta-1 is the human homologue of the Drosophila Delta protein that binds
CC to Notch protein. H-Delta-1 polypeptides can be used to treat or prevent
CC disorders characterised by increased Notch activity, such as cervical,
CC breast, lung or colon cancer, melanoma or seminoma, as well as nervous
CC system disorders, and to promote tissue regeneration and repair
XX
SQ Sequence 175 AA;
Query Match 98.1%; Score 908; DB 2; Length 175;
Best Local Similarity 99.4%; Pred. No. 9.9e-86;
Matches 174; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 TNNLANCQREKDISVSIIGATGIXNTNKKADFXXGDXSSDKNGFQKARYPSVDYNLVQD 60
DB 1 TNNLANCQREKDISVSIIGATGIXNTNKKADFXXGDXSSDKNGFQKARYPSVDYNLVQD 60
QY 61 LKGGDTAVRTSHSKRTKQSGSGRRRGRPHSGXACCGPGSGGTTGWSWNHCSVS 120
DB 61 LKGGDTAVRTSHSKRTKQSGSGRRRGRPHSGXACCGPGSGGTTGWSWNHCSVS 120
QY 121 LPKCSHAFIVDFLYPFPSGEASERKPDSCGTSKDTKYQSVVVISSEKDECVIA 175
DB 121 LPKCSHAFIVDFLYPFPSGEASERKPDSCGTSKDTKYQSVVVISSEKDECVIA 175
RESULT 2
AAW11721
ID AAW11721 standard; protein; 175 AA.
AC AAW11721;
XX
XX 28-APR-1997 (first entry)
XX
DE H-Delta-1 polypeptide (reading frame 1 product).
XX
KW H-Delta-1; cell proliferation; nervous system disorder;
KW tissue regeneration; Notch; cervix cancer; breast cancer; lung cancer;
KW colon cancer; melanoma; seminoma; neurogenesis; therapy.
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Misc-difference 4
FT /label= Gln, Stop
FT /note= "variable site resulting from degeneracy of the H-
FT delta-1 DNA sequence"
FT Misc-difference 22
FT /label= Tyr, His
FT /note= "variable site resulting from degeneracy of the H-
FT delta-1 DNA sequence"
FT Misc-difference 26
FT /label= Arg, Gly
FT /note= "variable site resulting from degeneracy of the H-
FT delta-1 DNA sequence"
FT Misc-difference 34
FT /note= "variable site resulting from degeneracy of the H-
FT delta-1 DNA sequence"
FT Misc-difference 35
FT /label= His, Gln
FT /note= "variable site resulting from degeneracy of the H-
FT delta-1 DNA sequence"
FT Misc-difference 39
FT /label= Ser, Arg
FT /note= "variable site resulting from degeneracy of the H-

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FT Misc-difference 56
FT /note= "residue 50 corresponds to a stop codon in the H-
FT Delta-1 DNA sequence"
FT Misc-difference 97
FT /label= Gly, Val
FT /note= "variable site resulting from degeneracy of the H-
FT delta-1 DNA sequence"
XX
PN WO9701571-A1.
XX
PD 16-JAN-1997.
XX
XX 28-JUN-1996; 96WO-US011178.
XX
XX 28-JUN-1995; 95US-0000589P.
XX
PA (IMCR ) IMPERIAL CANCER RES TECHNOLOGY.
PA (UYUA ) UNIV YALE.
XX
PI Ish-Horowicz D, Henrique D, Lewis J, Artavanis-Tsakonas S;
PI Gray GE;
XX
DR WPI: 1997-100159/09.
DR N-PSDB; AAT58900.
XX
XX New vertebrate Delta protein, DNA and antibodies - for treating and
XX preventing cancer, nervous system disorders and for tissue regeneration.
XX
PS Disclosure; Fig 10A-B; 135pp; English.
XX
CC Polypeptide sequences (AAW11721-23) were detd. for all 3 reading frames
CC of a human H-Delta-1 gene sequence (AAT58900) isolated from a genomic
CC library. No single reading frame gave the correct sequence owing to
CC errors that caused reading frame shifts. An alignment of the polypeptides
CC with that of chick C-delta-1 (AAW11719) allowed the correct H-Delta-1
CC sequence to be predicted (see also AAW11724). H-Delta-1 polypeptide
CC sequences (AAW11725-38) were also deduced from an H-Delta-1 contig
CC (AAT59454). Delta-1 proteins can be used to treat or prevent disorders
CC characterised by increased Notch activity, such as cervical, breast, lung
CC or colon cancer, melanoma or seminoma, as well as nervous system
CC disorders, and to promote tissue regeneration and repair
XX
SQ Sequence 175 AA;
Query Match 73.3%; Score 678.5; DB 2; Length 175;
Best Local Similarity 92.1%; Pred. No. 6.1e-62;
Matches 129; Conservative 1; Mismatches 9; Indels 1; Gaps 1;
QY 36 GDXSSDKNGFQKARYPSVDYNLVQDKGDDTAVRTSHSKRTKQSGSGRRRGRPHS 95
DB 37 GTXASDKNGFQ-GPLPQRLXLVQDLKGDDTAVRTSHSKRTKQSGSGRRRGRPHS 95
QY 96 GXACCGPGSGGTTGWSWNHCSVSLPKCSHAFIVDFLYPFPSGEASERKPDSCGTSK 155
DB 96 GXACCGPGSGGTTGWSWNHCSVSLPKCSHAFIVDFLYPFPSGEASERKPDSCGTSK 155
QY 156 DTKYQSVVVISSEKDECVIA 175
DB 156 DTKYQSVVVISSEKDECVIA 175
RESULT 3
AAW18349
ID AAW18349 standard; protein; 702 AA.
XX
AC AAW18349;
XX
XX 11-FEB-1998 (first entry)
XX
DE Proliferation and differentiation suppression polypeptide.
XX
KW Proliferation; differentiation; suppression; human; delta-1; serrate-1;

```

KW blood cell; neuron; leukaemia; malignant tumour; immunosuppression.  
 XX Homo sapiens.  
 OS WO9719172-A1.  
 PN 29-MAY-1997.  
 XX 15-NOV-1996; 96WO-JP003356.  
 PF 17-NOV-1995; 95JP-00299611.  
 PR 30-NOV-1995; 95JP-00311811.  
 XX (ASAH ) ASAH KASEI KOGYO KK.  
 PA Sakano S, Itoh A;  
 PI WPI; 1997-298110/27.  
 DR Peptide(s) encoded by human genes delta-1 and serrate-1 - suppress  
 PT proliferation and differentiation of undifferentiated human blood cells.  
 XX Claim 4; Page 61-64; 114pp; Japanese.  
 PS The present sequence represents a polypeptide which suppresses  
 CC proliferation and differentiation of undifferentiated cells such as  
 CC neurons and blood cells. The polypeptide may be used for the prevention  
 CC and control of disorders involving undifferentiated cells, such as  
 CC leukaemia and malignant tumours, and improvement of blood formation, e.g.  
 CC after immunosuppression  
 XX Sequence 702 AA;  
 SQ

Query Match 57.0%; Score 527.5; DB 2; Length 702;  
 Best Local Similarity 64.8%; Pred. No. 1.6e-45;  
 Matches 114; Conservative 4; Mismatches 13; Indels 45; Gaps 4;

QY 1 TNNLANCOREKDISVSIIGATGIXNTNKKADPXXGDXSSDKNGFQKARYPSVDYVNLVQD 60  
 DB 568 TNNLANCOREKDISVSIIGATGIXNTNKKADP-HGDHSADKNGF-KARYPAVDYVNLVQD 625  
 QY 61 LKGGDTAVRTSHSKRDTKCQSPGSSGRRRG-PRPHSGXACCGPGSGGGTGWVSSWNHCSV 119  
 DB 656 LKGGDTAVRTSHSKRDTKCQSPGSSGRRRG-PRPHSGXACCGPGSGGGTGWVSSWNHCSV 119  
 QY 120 SLPKCSHAFIVDFLYFPFSGEASERKRPDSCGTSKDTKYQSVYVISEKDECVIA 175  
 DB 663 -----GEASERKRPDSCGTSKDTKYQSVYVISEKDECVIA 699

RESULT 4  
 AAW75495  
 ID AAW75495 standard; protein; 702 AA.  
 AC AAW75495;  
 DT 27-APR-1999 (first entry)  
 DE Truncated human delta-1 protein #3.  
 KW Human; delta-1 protein; ligand; notch; drug; vascular cell; primer; PCR;  
 KW amplification; truncation.  
 OS Homo sapiens.  
 PN JP10316582-A.  
 PD 02-DEC-1998.  
 XX 14-MAY-1997; 97JP-00124062.  
 PR 14-MAY-1997; 97JP-00124062.  
 XX

PA (ASAH ) ASAH KASEI KOGYO KK.  
 XX WPI; 1999-076401/07.  
 DR Vascular cell controlling agent comprises polypeptide - which is human  
 PT notch ligand and is used as drug.  
 XX Claim 2; Page 14-16; 21pp; Japanese.  
 PS This sequence represents a truncated human delta-1 protein corresponding  
 CC to amino acids 1-702 of the mature protein (see AAW75492). The delta-1  
 CC protein is a ligand of the human notch protein and the protein or  
 CC fragments, especially AAW75493-W75495, can be used as a drug to control  
 CC vascular cells. The sequences were isolated and the truncated fragments  
 CC were generated using the primers AAX16818-X16831  
 XX Sequence 702 AA;  
 SQ

Query Match 57.0%; Score 527.5; DB 2; Length 702;  
 Best Local Similarity 64.8%; Pred. No. 1.6e-45;  
 Matches 114; Conservative 4; Mismatches 13; Indels 45; Gaps 4;

QY 1 TNNLANCOREKDISVSIIGATGIXNTNKKADPXXGDXSSDKNGFQKARYPSVDYVNLVQD 60  
 DB 568 TNNLANCOREKDISVSIIGATGIXNTNKKADP-HGDHSADKNGF-KARYPAVDYVNLVQD 625  
 QY 61 LKGGDTAVRTSHSKRDTKCQSPGSSGRRRG-PRPHSGXACCGPGSGGGTGWVSSWNHCSV 119  
 DB 656 LKGGDTAVRTSHSKRDTKCQSPGSSGRRRG-PRPHSGXACCGPGSGGGTGWVSSWNHCSV 119  
 QY 120 SLPKCSHAFIVDFLYFPFSGEASERKRPDSCGTSKDTKYQSVYVISEKDECVIA 175  
 DB 663 -----GEASERKRPDSCGTSKDTKYQSVYVISEKDECVIA 699

RESULT 5  
 AAW18353  
 ID AAW18353 standard; protein; 723 AA.  
 AC AAW18353;  
 DT 11-FEB-1998 (first entry)  
 DE Proliferation and differentiation suppression polypeptide.  
 KW Proliferation; differentiation; suppression; human; delta-1; serrate-1;  
 KW blood cell; neuron; leukaemia; malignant tumour; immunosuppression.  
 XX Homo sapiens.  
 FH Key Location/Qualifiers  
 FT Peptide 1..21  
 FT Protein /label= Signal  
 FT Protein /label= Differentiation\_suppression\_protein  
 XX WO9719172-A1.  
 PN 29-MAY-1997.  
 XX 15-NOV-1996; 96WO-JP003356.  
 PF 17-NOV-1995; 95JP-00299611.  
 PR 30-NOV-1995; 95JP-00311811.  
 XX (ASAH ) ASAH KASEI KOGYO KK.  
 PA Sakano S, Itoh A;  
 PI WPI; 1997-298110/27.  
 DR N-PSDB; AAT70174.  
 XX Peptide(s) encoded by human genes delta-1 and serrate-1 - suppress  
 PT

PT proliferation and differentiation of undifferentiated human blood cells.  
 XX  
 PS Claim 15; Page 77-82; 114pp; Japanese.  
 XX  
 CC The present sequence represents a polypeptide which suppresses  
 CC proliferation and differentiation of undifferentiated cells such as  
 CC neurons and blood cells. The polypeptide may be used for the prevention  
 CC and control of disorders involving undifferentiated cells, such as  
 CC leukaemia and malignant tumours, and improvement of blood formation, e.g.  
 CC after immunosuppression  
 XX  
 SQ Sequence 723 AA;  
 Query Match 57.0%; Score 527.5; DB 2; Length 723;  
 Best Local Similarity 64.8%; Pred. No. 1.6e-45;  
 Matches 114; Conservative 4; Mismatches 13; Indels 45; Gaps 4;  
 QY 1 TNNLANCQREKDISVSIIGATGIXNTNKKADFXGXGSDXKNGFQKARYPSVDYNLVQD 60  
 DB 589 TNNLANCQREKDISVSIIGATGIXNTNKKADFXGXGSDXKNGF-KARYPAVDYNLVQD 646  
 QY 61 LKGGDTAVRTSHSKRDTKQSPGSSGRRRG-PRPHSGXACCGPGSGGTGWGVSSWNHCSV 119  
 DB 647 LKGGDTAVRDAHSKRDTKQSPGSSGEGKGTPTTLRG----- 683  
 QY 120 SLPKCSHAFIVDFLYPFPSGEASERKRPDSCGSGTSDTKYQSVYVISEKDECVIA 175  
 DB 684 -----GEASERKRPDSCGSGTSDTKYQSVYVISEKDECVIA 720  
 RESULT 6  
 AAW75492  
 ID AAW75492 standard; protein; 723 AA.  
 XX  
 AC AAW75492;  
 DT 27-APR-1999 (first entry)  
 XX  
 DE Human delta-1 protein.  
 XX  
 KW Human; delta-1 protein; ligand; notch; drug; vascular cell; primer; PCR;  
 KW amplification.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT Peptide 1..21  
 FT /notes="signal peptide"  
 FT Protein 22..723  
 FT /notes="mature delta-1 protein"  
 XX  
 PN JP10316582-A.  
 XX  
 PD 02-DEC-1998.  
 XX  
 PF 14-MAY-1997; 97JP-00124062.  
 XX  
 PR 14-MAY-1997; 97JP-00124062.  
 XX  
 PA (ASAH ) ASahi KASEI KOGYO KK.  
 XX  
 DR WPI: 1999-076401/07.  
 DR N-PSDB; AAW16817.  
 XX  
 PT Vascular cell controlling agent comprises polypeptide - which is human  
 PT notch ligand and is used as drug.  
 PS  
 PS Disclosure; Page 16-19; 21pp; Japanese.  
 XX  
 CC This sequence represents the human delta-1 protein, which is a ligand of  
 CC the human notch protein. The protein or fragments, especially AAW75493-  
 CC W75495, can be used as a drug to control vascular cells. The sequences  
 CC were isolated and the truncated fragments were generated using the

CC primers AAX16818-X16831  
 XX  
 SQ Sequence 723 AA;  
 Query Match 57.0%; Score 527.5; DB 2; Length 723;  
 Best Local Similarity 64.8%; Pred. No. 1.6e-45;  
 Matches 114; Conservative 4; Mismatches 13; Indels 45; Gaps 4;  
 QY 1 TNNLANCQREKDISVSIIGATGIXNTNKKADFXGXGSDXKNGFQKARYPSVDYNLVQD 60  
 DB 589 TNNLANCQREKDISVSIIGATGIXNTNKKADFXGXGSDXKNGF-KARYPAVDYNLVQD 646  
 QY 61 LKGGDTAVRTSHSKRDTKQSPGSSGRRRG-PRPHSGXACCGPGSGGTGWGVSSWNHCSV 119  
 DB 647 LKGGDTAVRDAHSKRDTKQSPGSSGEGKGTPTTLRG----- 683  
 QY 120 SLPKCSHAFIVDFLYPFPSGEASERKRPDSCGSGTSDTKYQSVYVISEKDECVIA 175  
 DB 684 -----GEASERKRPDSCGSGTSDTKYQSVYVISEKDECVIA 720  
 RESULT 7  
 AAW94498  
 ID AAW94498 standard; protein; 723 AA.  
 XX  
 AC AAW94498;  
 DT 22-APR-1999 (first entry)  
 XX  
 DE Human delta-1 protein.  
 XX  
 KW Human; delta-1; delta-2; differentiation inhibitor; proliferation;  
 KW leukaemia; malignant tumour.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT Peptide 1..21  
 FT /label="signal  
 FT Protein 22..723  
 FT /label="Delta-1  
 XX  
 PN WO9851799-A1.  
 XX  
 PD 19-NOV-1998.  
 XX  
 PF 13-MAY-1998; 98WO-JP002104.  
 XX  
 PR 14-MAY-1997; 97JP-00124064.  
 XX  
 PA (ASAH ) ASahi KASEI KOGYO KK.  
 XX  
 PI Sakano S;  
 XX  
 DR WPI: 1999-070120/06.  
 DR N-PSDB; AAX16300.  
 XX  
 PT Peptide inhibiting the differentiation of undifferentiated blood - used  
 PT for treatment of cancer and other disorders and the culture of human  
 PT cells in vitro.  
 XX  
 PS Example 1; Page 64-69; 86pp; Japanese.  
 XX  
 CC The present invention describes full length and shortened human delta-2  
 CC proteins. Human delta-2 is a differentiation inhibitor which inhibits the  
 CC differentiation of undifferentiated cells (other than brain or muscle  
 CC cells), such as blood cells, and enhances the proliferation of  
 CC undifferentiated blood cells. Products of human delta-2 may be used for  
 CC the treatment of diseases such as leukaemia and malignant tumours. They  
 CC may also be used in the culture of human cells in vitro, e.g. for  
 CC production of supplies of undifferentiated blood cells. The present  
 CC sequence represents human delta-1, from an example of the present  
 CC invention

```
XX SQ Sequence 723 AA;
Query Match 57.0%; Score 527.5; DB 2; Length 723;
Beat Local Similarity 64.8%; Pred. No. 1.6e-45;
Matches 114; Conservative 4; Mismatches 13; Indels 45; Gaps 4;
QY 1 TNNNLANCOREKDISVSIIGATGIKNTNKKADPFXXGDXSSDKNGFKQARYPSVDYNLVQD 60
Db TNNNLANCOREKDISVSIIGATGIKNTNKKADPF-HGHSADKNGF-KARYPAVDYNLVQD 646
QY 61 LKGDPTAVRTSHSKRDTKCQSPGSSGRRRG-PRPHSGXACCGPGSGGGTGWGVSSWNHCSV 119
Db LKGDPTAVRTSHSKRDTKCQSPGSSGRRRG-PRPHSGXACCGPGSGGGTGWGVSSWNHCSV 119
QY 647 LKGDPTAVRTSHSKRDTKCQSPGSSGRRRG-PRPHSGXACCGPGSGGGTGWGVSSWNHCSV 175
Db LKGDPTAVRTSHSKRDTKCQSPGSSGRRRG-PRPHSGXACCGPGSGGGTGWGVSSWNHCSV 175
QY 120 SLPKCSHAFIVDFLPFPGSGEASERKRPDPGSGSTSKDTKYQSVYVISEKDECVIA 175
Db SLPKCSHAFIVDFLPFPGSGEASERKRPDPGSGSTSKDTKYQSVYVISEKDECVIA 175
QY 684 -----GEASERKRPDPGSGSTSKDTKYQSVYVISEKDECVIA 720
Db -----GEASERKRPDPGSGSTSKDTKYQSVYVISEKDECVIA 720

RESULT 8
ID AAY83227 standard; protein; 723 AA.
AC AAY83227;
DT 16-AUG-2000 (first entry)
XX PRO172 Polypeptide.
DE Inhibition; cancer; neoplasia; tumour; breast; ovary; renal; colorectal;
KW uterus; prostate; lung; bladder; central nervous system; CNS; melanoma;
KW leukaemia; PRO211; PRO228; PRO338; PRO172; PRO182; human.
XX Homo sapiens.
XX Key Location/Qualifiers
PH Peptide 1..21
FT label= Signal_peptide
FT 2..8
FT /note= "N-myristoylation site"
FT Modified-site 37..43
FT /note= "N-myristoylation site"
FT Modified-site 40..46
FT /note= "N-myristoylation site"
FT Modified-site 93..97
FT /note= "Casein kinase II phosphorylation site"
FT Modified-site 98..104
FT /note= "N-myristoylation site"
FT Modified-site 99..105
FT /note= "N-myristoylation site"
FT Modified-site 131..135
FT /note= "Casein kinase II phosphorylation site"
FT Modified-site 154..158
FT /note= "Casein kinase II phosphorylation"
FT Modified-site 176..185
FT /note= "Tyrosine kinase phosphorylation site"
FT Modified-site 203..207
FT /note= "Casein kinase II phosphorylation site"
FT Domain 243..255
FT /label= EGF-like_domain
FT Modified-site 252..261
FT /note= "Tyrosine kinase phosphorylation site"
FT Modified-site 262..268
FT /note= "N-myristoylation site"
FT Domain 274..286
FT /note= "EGF-like domain"
FT Modified-site 281..287
FT /note= "N-myristoylation site"
FT Modified-site 282..288
FT /note= "N-myristoylation site"
FT Modified-site 301..307
FT /note= "N-myristoylation site"
FT 310..316
FT /note= "N-myristoylation site"
FT Domain 314..326
FT /label= EGF-like_domain
FT Modified-site 328..334
FT /note= "N-myristoylation domain"
FT Modified-site 340..346
FT /note= "N-myristoylation site"
FT Modified-site 342..346
FT /note= "Casein kinase II phosphorylation site"
FT Modified-site 343..355
FT /note= "Asn and Asp hydroxylation site"
FT Modified-site 344..348
FT /note= "Casein kinase II phosphorylation site"
FT Domain 352..364
FT /label= EGF-like_domain
FT Modified-site 369..373
FT /note= "Casein kinase II phosphorylation site"
FT Modified-site 378..384
FT /note= "N-myristoylation site"
FT Modified-site 387..393
FT /note= "N-myristoylation site"
FT Domain 391..403
FT /label= EGF-like_domain
FT Modified-site 420..432
FT /note= "Asn and Asp hydroxylation site"
FT Domain 429..441
FT /label= EGF-like_domain
FT Modified-site 457..461
FT /note= "Casein kinase II phosphorylation site"
FT Modified-site 458..480
FT /label= Asn and Asp hydroxylation site
FT Domain 467..479
FT /label= EGF-like_domain
FT Modified-site 477..481
FT /note= "N-glycosylation site"
FT Modified-site 483..487
FT /note= "Casein kinase II phosphorylation site"
FT Modified-site 495..499
FT /note= "Casein kinase II phosphorylation site"
FT Domain 505..517
FT /label= EGF-like_domain
FT Modified-site 512..518
FT /note= "N-myristoylation site"
FT Domain 548..568
FT /label= Transmembrane_domain
FT Binding-site 552..563
FT /label= Prokaryotic membrane lipoprotein lipid attachment
FT Modified-site 559..563
FT /note= "Casein kinase II phosphorylation site"
FT Modified-site 600..604
FT /note= "cAMP and cGMP dependent protein kinase phosphorylation site"
FT Modified-site 670..674
FT /note= "Casein kinase II phosphorylation site"
FT Modified-site 671..675
FT /note= "Casein kinase II phosphorylation site"
FT Modified-site 676..682
FT /note= "N-myristoylation site"
FT Modified-site 683..689
FT /note= "N-myristoylation site"
FT Modified-site 695..701
FT /note= "N-myristoylation site"
FT Modified-site 698..702
FT /note= "Casein kinase II phosphorylation site"
XX WO200021996-A2.
XX 20-APR-2000.
XX 05-OCT-1999; 99WO-US023089.
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PR 13-OCT-1998; 98US-0104080P.
XX
XX (GETH ) GENENTECH INC.
XX
XX Ashkenazi A, Goddard A, Gurney AL, Klein RD, Napier M, Wood WI;
XX Yuan J;
XX
XX WPI; 2000-317943/27.
XX N-PSDB; AA293703.
XX
XX Composition for inhibiting neoplastic cell growth and treating cancers of
XX PT ovary, uterus, prostate, lung and bladder, comprises PRO211, PRO228,
XX PRO538, PRO172 or PRO182 polypeptide or their agonist.
XX
XX Claim 12; Fig 8; 122pp; English.
XX
XX Compositions comprising a PRO211, PRO228, PRO538, PRO172 or PRO182
XX polypeptide or their agonists, mixed with a carrier is useful for
XX inhibiting neoplastic growth and treating tumors such as cancers of
XX breast, ovary, renal, colorectal, uterus, prostate, lung, bladder,
XX central nervous system, melanoma and leukaemia
XX
XX Sequence 723 AA;
XX
XX Query Match 57.0%; Score 527.5; DB 3; Length 723;
XX Best Local Similarity 64.8%; Pred. No. 1.6e-45;
XX Matches 114; Conservative 4; Mismatches 13; Indels 45; Gaps 4;
XX
QY 1 TMNLANCQREKDISVSIIGATGIXNTNKKADFPXGDXSDXNGFQKARYPSVDYNLVQD 60
DQ 589 TMNLANCQREKDISVSIIGATGIXNTNKKADFPXGDXSDXNGFQKARYPSVDYNLVQD 646
QY 61 LKGGDTAVRTSHSKRTKQSPGSGRRRG-PRPHSGXACCGPGSGGTGWSMNHCSV 119
DQ 647 LKGGDTAVRDAHSKRTKQSPGSGRRRG-PRPHSGXACCGPGSGGTGWSMNHCSV 683
QY 120 SLPKCSHAFIVDPLYPFSGEASERKPDGSGTSDTKYQSVYVISEKDECVIA 175
DQ 684 -----GEASERKRPDGGSGTSDTKYQSVYVISEKDECVIA 720
XX
RESULT 9
AAB33422
ID AAB33422 standard; protein; 723 AA.
XX
XX AAB33422;
XX
XX 29-JAN-2001 (first entry)
XX
XX Human PRO172 protein UNQ146 SEQ ID NO:41.
XX
XX Human; immune related disease; diagnosis; antiinflammatory; cardiant;
XX dermatologic; antiarthritic; antirheumatic; immunosuppressive;
XX haemostatic; antithyroid; antidiabetic; neurotropic; neuroprotective;
XX antianemic; hepatocytic; virucide; antipsoriatic; antiallergic;
XX antiasthmatic; systemic lupus erythematosus; rheumatoid arthritis;
XX osteoarthritis; spondyloarthritis; systemic sclerosis; sarcoidosis;
XX idiopathic inflammatory myopathy; Sjogren's syndrome; thyroiditis;
XX systemic vasculitis; autoimmune haemolytic anaemia; diabetes mellitus;
XX autoimmune thrombocytopaenia; immune-mediated renal disease;
XX demyelinating disease; hepatobiliary disease; Whipple's disease;
XX inflammatory bowel disease; gluten-sensitive enteropathy;
XX autoimmune disease; immune-mediated skin disease; allergic disease;
XX immunologic disease; transplantation associated disease;
XX graft rejection; graft-versus-host-disease.
XX
XX Homo sapiens.
XX
XX WO2000053758-A2.
XX
XX 14-SEP-2000.
XX
XX 02-MAR-2000; 2000WO-US005841.
```

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XX
XX 08-MAR-1999; 99WO-US005028.
XX 10-MAR-1999; 99US-0123618P.
XX 12-MAR-1999; 99US-0123957P.
XX 23-MAR-1999; 99US-0125775P.
XX 12-APR-1999; 99US-0128849P.
XX 20-APR-1999; 99WO-US008615.
XX 28-APR-1999; 99US-0134445P.
XX 04-MAY-1999; 99US-0134287P.
XX 02-JUN-1999; 99WO-US012252.
XX 23-JUN-1999; 99US-0141037P.
XX 20-JUL-1999; 99US-0144758P.
XX 26-JUL-1999; 99US-0145698P.
XX 28-JUL-1999; 99US-0146222P.
XX 01-SEP-1999; 99WO-US020111.
XX 08-SEP-1999; 99WO-US020594.
XX 13-SEP-1999; 99WO-US020944.
XX 15-SEP-1999; 99WO-US021090.
XX 15-SEP-1999; 99WO-US021547.
XX 05-OCT-1999; 99WO-US023089.
XX 29-OCT-1999; 99US-0162506P.
XX 29-NOV-1999; 99WO-US028214.
XX 30-NOV-1999; 99WO-US028313.
XX 30-NOV-1999; 99WO-US028409.
XX 01-DEC-1999; 99WO-US028301.
XX 01-DEC-1999; 99WO-US028634.
XX 02-DEC-1999; 99WO-US028551.
XX 02-DEC-1999; 99WO-US028564.
XX 16-DEC-1999; 99WO-US030095.
XX 20-DEC-1999; 99WO-US030999.
XX 30-DEC-1999; 99WO-US031274.
XX 05-JAN-2000; 2000WO-US000219.
XX 06-JAN-2000; 2000WO-US000277.
XX 06-JAN-2000; 2000WO-US000376.
XX 11-FEB-2000; 2000WO-US003565.
XX 18-FEB-2000; 2000WO-US004341.
XX 18-FEB-2000; 2000WO-US004342.
XX 22-FEB-2000; 2000WO-US004414.
XX
XX (GETH ) GENENTECH INC.
XX
XX Ashkenazi AJ, Baker KP, Goddard A, Gurney AL, Hebert C, Henzel W;
XX Kabakoff RC, Lu Y, Pan J, Pennica D, Shelton DL, Smith V;
XX Stewart TA, Tumas D, Watanabe CK, Wood WI, Yan M;
XX
XX WPI; 2000-572271/53.
XX N-PSDB; AAC58587.
XX
XX Sixty four PRO polypeptides, useful in the diagnosis and treatment of
XX immune related disorders, e.g. systemic lupus erythematosus, rheumatoid
XX arthritis, osteoarthritis, thyroiditis and diabetes mellitus.
XX
XX Claim 33; Fig 18; 309pp; English.
XX
XX The present invention describes sixty four human PRO proteins which can
XX be used in the treatment of immune related diseases. The human PRO
XX proteins, anti-PRO antibodies, agonists and antagonists are useful for
XX treating and diagnosing immune related disorders. The disorders are
XX selected from systemic lupus erythematosus, rheumatoid arthritis,
XX osteoarthritis, juvenile chronic arthritis, spondyloarthritis,
XX systemic sclerosis, idiopathic inflammatory myopathies, Sjogren's
XX syndrome, systemic vasculitis, sarcoidosis, autoimmune haemolytic
XX anaemia, autoimmune thrombocytopaenia, thyroiditis, diabetes mellitus,
XX immune-mediated renal disease, demyelinating diseases of the central and
XX peripheral nervous systems, hepatobiliary diseases, inflammatory bowel
XX disease, gluten-sensitive enteropathy and Whipple's disease, autoimmune
XX or immune-mediated skin diseases, allergic diseases, immunological
XX diseases of the lung, and transplantation associated diseases including
XX graft rejection and graft-versus-host-disease. AAC58397 to AAC58578
XX represent PCR primers and hybridisation probes used in the isolation of
XX human PRO sequences. AAC58579 to AAC58642 and AAB33414 to AAB33477
```



CC represent human PRO polynucleotide and protein sequences given in the  
 CC exemplification of the present invention  
 XX  
 SQ Sequence 723 AA;

Query Match 57.0%; Score 527.5; DB 3; Length 723;  
 Best Local Similarity 64.8%; Pred. No. 1.6e-45;  
 Matches 114; Conservative 4; Mismatches 13; Indels 45; Gaps 4;

QY 1 TNNNLANCOREKDISVSIIGATGIXNTNKKADFFXGDXSSDKNGFQKARYPSVDYNLVQD 60  
 DB 589 TNNNLANCOREKDISVSIIGATGIXNTNKKADFFXGDXSSDKNGFQKARYPSVDYNLVQD 646  
 QY 61 LKGGDTAVRTSHSKRDTKQSPGSGRRRG-PRPHSGXACCGPGSGGGTGWVSSNNHCSV 119  
 DB 647 LKGGDTAVRDASHKRDTHKQPGSGGEEKGTPTTLRG----- 683

QY 120 SLPKCSHAFIVDFLYFPFSGEASERKRPDSCGSTSKDTKYQSVYVISEKDECVIA 175  
 DB 684 -----GEASERKRPDSCGSTSKDTKYQSVYVISEKDECVIA 720

RESULT 10  
 AAB24388  
 ID AAB24388 standard; protein; 723 AA.  
 XX  
 AC AAB24388;  
 XX  
 DT 07-NOV-2000 (first entry)  
 XX  
 DE Human PRO172 protein sequence SEQ ID NO:4.  
 XX  
 KW Human; PRO; promotion; inhibition; angiogenesis; cardiovascularisation;  
 KW diagnosis; trauma; wound; cancer; atherosclerosis; cardiac hypertrophy;  
 KW angiogenic; proliferative; cardiac; cardiovascular; antiatherosclerotic;  
 KW cytostatic; gene therapy; vaccine.  
 XX  
 OS Homo sapiens.  
 XX  
 FN WO200032221-A2.  
 XX  
 PD 08-JUN-2000.  
 XX  
 PF 30-NOV-1999; 99WO-US028313.  
 XX  
 PR 01-DEC-1998; 98WO-US025108.  
 PR 16-DEC-1998; 98US-0112850P.  
 PR 12-JAN-1999; 99US-0115554P.  
 PR 08-MAR-1999; 99WO-US005028.  
 PR 12-MAR-1999; 99US-0123957P.  
 PR 28-APR-1999; 99US-0131445P.  
 PR 14-MAY-1999; 99US-0134287P.  
 PR 02-JUN-1999; 99WO-US012252.  
 PR 23-JUN-1999; 99US-0141037P.  
 PR 20-JUL-1999; 99US-0144758P.  
 PR 26-JUL-1999; 99US-0145698P.  
 PR 01-SEP-1999; 99WO-US020111.  
 PR 08-SEP-1999; 99WO-US020594.  
 PR 13-SEP-1999; 99WO-US020944.  
 PR 15-SEP-1999; 99WO-US021090.  
 PR 15-SEP-1999; 99WO-US021547.  
 PR 05-OCT-1999; 99WO-US023089.  
 PR 29-OCT-1999; 99US-0162508P.  
 XX  
 PA (GETH ) GENENTECH INC.  
 XX  
 PI Ashkenazi AJ, Baker KP, Ferrara N, Gerber H, Hillan KJ;  
 PI Goddard A, Godowski PJ, Gurney AL, Klein RD, Kuo SS, Paoni NF;  
 PI Smith V, Watanabe CK, Williams PM, Wood WI;  
 XX  
 DR WPI; 2000-412154/35.  
 DR N-PSDB; AAA77512.  
 XX

PT Nucleic acids encoding PRO polypeptides useful for preventing, diagnosing  
 PT and treating diagnosing a cardiovascular, endothelial or angiogenic  
 XX disorders in mammals.  
 PS Claim 72; Fig 2; 315pp; English.  
 XX The present invention describes nucleic acids encoding PRO polypeptides  
 CC useful for preventing, diagnosing and treating diagnosing a  
 CC cardiovascular, endothelial or angiogenic disorder in mammals by  
 CC modulating cell proliferation, angiogenesis and cardiovascularisation,  
 CC and for identifying agonists and antagonists of these processes. The  
 CC nucleic acids and the proteins they encode may be used in the prevention,  
 CC treatment and diagnosis of diseases associated with inappropriate PRO  
 CC expression such as cardiovascular, endothelial or angiogenic disorders in  
 CC mammals (e.g. atherosclerosis, cancers and cardiac hypertrophy). For  
 CC example, the nucleic acids (Nc) and vectors containing them and the PRO  
 CC polypeptide may be used to treat disorders associated with decreased PRO  
 CC expression. AAA77510 to AAA77721 and AAB24388 to AAB24435 represent  
 CC nucleotide and protein sequences used in the exemplification of the  
 CC present invention  
 XX  
 SQ Sequence 723 AA;

Query Match 57.0%; Score 527.5; DB 3; Length 723;  
 Best Local Similarity 64.8%; Pred. No. 1.6e-45;  
 Matches 114; Conservative 4; Mismatches 13; Indels 45; Gaps 4;

QY 1 TNNNLANCOREKDISVSIIGATGIXNTNKKADFFXGDXSSDKNGFQKARYPSVDYNLVQD 60  
 DB 589 TNNNLANCOREKDISVSIIGATGIXNTNKKADFFXGDXSSDKNGFQKARYPSVDYNLVQD 646  
 QY 61 LKGGDTAVRTSHSKRDTKQSPGSGRRRG-PRPHSGXACCGPGSGGGTGWVSSNNHCSV 119  
 DB 647 LKGGDTAVRDASHKRDTHKQPGSGGEEKGTPTTLRG----- 683

QY 120 SLPKCSHAFIVDFLYFPFSGEASERKRPDSCGSTSKDTKYQSVYVISEKDECVIA 175  
 DB 684 -----GEASERKRPDSCGSTSKDTKYQSVYVISEKDECVIA 720

RESULT 11  
 AA79032  
 ID AA79032 standard; protein; 723 AA.  
 XX  
 AC AA79032;  
 XX  
 DT 06-JUN-2000 (first entry)  
 XX  
 DE Human delta protein amino acid sequence.  
 XX  
 KW Delta; Kuz; Notch; differentiation; cervical; breast; colon; cancer;  
 KW lung; melanoma; seminoma; central nervous system disorder; psoriasis;  
 KW tissue regeneration; liver cirrhosis; keloid formation; baldness;  
 XX inner ear disorder; human.  
 OS Homo sapiens.  
 XX  
 FN WO200002897-A2.  
 XX  
 PD 20-JAN-2000.  
 XX  
 PF 13-JUL-1999; 99WO-US015817.  
 XX  
 PR 13-JUL-1998; 98US-0092513P.  
 PR 19-OCT-1998; 98US-0104834P.  
 XX  
 PA (UYVA ) UNIV YALE.  
 XX  
 PI Artavanis-Tsakonas S, Rand MD, Qi H;  
 XX  
 DR WPI; 2000-282852/24.  
 DR N-PSDB; AAZ98679.  
 XX

PT New cleavage peptide, nucleic acids and antibodies useful for diagnosis,  
PT prevention and treatment of cancer, disorders of central nervous system,  
PT cirrhosis and psoriasis.

XX Claim 1; Fig 4; 177pp; English.

XX  
PS  
PS  
CC This sequence represents the human delta protein amino acid sequence.  
CC Delta is a topolythmic protein that contains a sequence which is cleaved  
CC by the metalloprotease-disintegrin kuzbanian (Kuz). Cleavage by Kuz  
CC results in two fragments, a soluble amino terminal fragment consisting  
CC essentially of the extracellular domain, and a membrane bound fragment  
CC consisting of the transmembrane domain and the intracellular domain. The  
CC soluble fragment is able to bind to Notch. Delta plays a key role in  
CC differentiation, and therefore detection and measurement of delta  
CC activation is important in the study of differentiation. The invention  
CC relates to the delta cleavage peptides (the active fragment), and to  
CC methods for detecting and measuring delta activation. Delta cleavage  
CC peptides, and chimeric proteins are useful for modulating the activity of  
CC Notch, delta or kuz or at least one of the signalling pathways in a cell  
CC or organism, expressing Notch. By contacting a cell with kuz protein or  
CC nucleic acid or its antibody, the activity or levels of delta protein is  
CC modulated and vice versa. A delta cleavage peptide or its derivative  
CC capable of binding kuz protein is useful for treating or preventing a  
CC disease or disorder associated with increased delta activity or  
CC expression such as cervical, breast, colon or lung cancer, melanoma or  
CC seminoma in humans. A recombinant cell comprising a delta peptide is  
CC useful for treating or preventing central nervous system disorders. A  
CC delta cleavage peptide is useful for the diagnosis of diseases or  
CC disorders associated with increased levels of Notch-delta protein binding  
CC activity comprising measuring the ability of delta cleavage peptides in a  
CC sample to bind kuz protein. A complex of delta protein and kuz is useful  
CC for diagnosing or screening for the presence of, or predisposition to  
CC developing a disease or disorder associated with aberrant levels of the  
CC complex, comprising measuring the level or functional activity of the  
CC complex or RNA encoding delta or kuz in a sample. The delta cleavage  
CC peptide is also useful for promoting tissue regeneration and repair, for  
CC treating liver cirrhosis, keloid formation, psoriasis, baldness and  
CC degenerative or traumatic disorders of the sensory epithelium of the  
CC inner ear

XX SQ Sequence 723 AA;

Query Match 57.0%; Score 527.5; DB 3; Length 723;  
Best Local Similarity 64.8%; Pred.No.1.6e-45;  
Matches 114; Conservative 4; Mismatches 13; Indels 45; Gaps 4;

QY 1 TNNLANCQREKDISVSIIGATQIKNTNKKADPFXGDXSSDKNGFQKARYPSVDYNLVQD 60  
|||||  
Db 589 TNNLANCQREKDISVSIIGATQIKNTNKKADP-HGDHSADKNGF-KARYPAVDYNLVQD 646  
|||||

QY 61 LKGGDTAVRTSHSKRTKQSPGSGRRRG-PRPHSGXACCGPGSGGGTGWSSWNHCSV 119  
|||||  
Db 647 LKGGDTAVRDAHSKRTKQSPGSGRRRG-PRPHSGXACCGPGSGGGTGWSSWNHCSV 119  
|||||

QY 120 SLPKCSHAFIVFLYFPFPGSEASERKPPSGGTSKDTKYQSVYVISEBKDECVIA 175  
|||||  
Db 684 -----GEASERKPPSGGTSKDTKYQSVYVISEBKDECVIA 720  
|||||

RESULT 12

AAB00172

ID AAB00172 standard; protein; 723 AA.

XX AAB00172;

DT 08-FEB-2001 (first entry)

DE PRO172 polypeptide.

XX PRO211; PRO228; PRO538; PRO172; PRO182; neoplasia; inhibition; tumour;  
KW treatment; therapy; agonist; antibody; breast cancer; ovarian cancer;  
KW renal cancer; colorectal cancer; uterine cancer; prostate cancer;  
KW lung cancer; bladder cancer; melanoma; leukaemia; inflammatory disorder;

KW angiogenic disorder; immunologic disorder; human.  
XX  
OS Homo sapiens.  
XX  
FH Key  
FT Peptide  
FT 1..21 Location/Qualifiers  
FT /label= Signal peptide  
FT 2..8  
FT /note= "N-myristoylation site"  
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FT /note= "Casein kinase II phosphorylation site"  
FT 98..104  
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FT 99..105  
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FT 154..158  
FT /note= "Casein kinase II phosphorylation site"  
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FT 243..255  
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FT 252..261  
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FT 262..268  
FT /note= "N-myristoylation site"  
FT 274..286  
FT /label= EGF-like domain cysteine pattern signatur  
FT 281..287  
FT /note= "N-myristoylation site"  
FT 282..288  
FT /note= "N-myristoylation site"  
FT 301..307  
FT /note= "N-myristoylation site"  
FT 310..316  
FT /note= "N-myristoylation site"  
FT 314..326  
FT /label= EGF-like domain cysteine pattern signatur  
FT 328..334  
FT /note= "N-myristoylation site"  
FT 340..346  
FT /note= "N-myristoylation site"  
FT 342..346  
FT /note= "Casein kinase II phosphorylation site"  
FT 343..355  
FT /note= "Asx hydroxylation site"  
FT 344..348  
FT /note= "Casein kinase II phosphorylation site"  
FT 352..364  
FT /note= "EGF-like domain cysteine pattern signatur"  
FT 369..373  
FT /note= "Casein kinase II phosphorylation site"  
FT 378..384  
FT /note= "N-myristoylation site"  
FT 387..393  
FT /note= "N-myristoylation site"  
FT 391..403  
FT /label= EGF-like domain cysteine pattern signatur  
FT 420..432  
FT /note= "Asx hydroxylation site"  
FT 429..441  
FT /label= EGF-like domain cysteine pattern signatur  
FT 457..461  
FT /note= "Casein kinase II phosphorylation site"  
FT 458..480  
FT /note= "Asx hydroxylation site"





CC nucleic acids, PRO proteins, antibodies against PRO proteins, PRO  
 CC agonists and PRO antagonists may be used as therapeutic agents to treat  
 CC cardiovascular, endothelial or angiogenic disorders, such as  
 CC atherosclerosis, osteoporosis, myocardial infarction, hypertension,  
 CC diabetic retinopathy, rheumatoid arthritis, Crohn's disease, psoriasis,  
 CC endometriosis, ulcers, wounds, cancer, Alzheimer's disease, Huntington's  
 CC disease, or stroke. PRO nucleic acids are additionally useful in the  
 CC recombinant production of PRO proteins, as hybridization probes to screen  
 CC libraries to isolate cDNAs with sequence identity to PRO proteins, to map  
 CC genes encoding PRO proteins, to analyse genetic disorders, and in gene  
 CC therapy. PRO nucleic acids can also be used to produce transgenic animals  
 CC useful for the development and screening of potential therapeutic agents.  
 CC The present sequence represents a PRO protein of the invention  
 XX  
 XX Sequence 723 AA;  
 SQ

Query Match 57.0%; Score 527.5; DB 4; Length 723;  
 Best Local Similarity 64.8%; Pred. NO. 1.6e-45;  
 Matches 114; Conservative 4; Mismatches 13; Indels 45; Gaps 4;

QY 1 TWNNLANCOREKDISVSIIGATGIXNTKKAFFXGDXSSDKNGFQKARYPSVDYNLVOD 60  
 Db 589 TWNNLANCOREKDISVSIIGATGIXNTKKAFF-HGDHSAKNGF-KARYPAVDYNLVOD 646

QY 61 LKGGDTAVRTSHSKRTKQSPGSGRRRG-PRPHSGXACCGPGSGGTGWGVSMNHCSV 119  
 Db 647 LKGGDTAVRDASHKRTKQCPQSGSGEKGTPTLRG----- 683

QY 120 SLPKCSHAFIVFLYPPFSGEASERKRPDSCGTSKDTKYQSVYVISEKDECVIA 175  
 Db 684 -----GEASERKRPDSCGTSKDTKYQSVYVISEKDECVIA 720

RESULT 15  
 ABO17788  
 ID ABO17788 standard; protein; 723 AA.  
 XX  
 AC ABO17788;  
 XX  
 DT 26-AUG-2003 (first entry)  
 XX  
 DE Novel human secreted and transmembrane protein PRO172.  
 KW Human; secreted and transmembrane protein; PRO; antinflammatory;  
 KW antiarteriosclerotic; cardiant; anti-infertility; anti-HIV; cytostatic;  
 KW antidiabetic; gene therapy; tumour necrosis factor (TNF)-alpha release;  
 KW TNF-alpha release; cell proliferation; cell differentiation;  
 KW gene expression modulator; proteoglycan release; cytokine release;  
 KW tumour; inflammatory disease; organ failure; atherosclerosis;  
 KW cardiac injury; infertility; birth defect; premature aging; AIDS;  
 KW acquired immunodeficiency syndrome; cancer; diabetic complication;  
 KW chromosome mapping; gene mapping; pharmaceutical; diagnostic; biosensor;  
 KW bio-reactor; tissue typing.  
 XX  
 OS Homo sapiens.  
 XX  
 PN US2003032156-A1.  
 XX  
 PD 13-FEB-2003.  
 XX  
 PF 06-MAY-2002; 2002US-00140474.  
 XX  
 PR 31-MAR-1997; 97WO-US005230.  
 PR 12-JUN-1998; 98WO-US012456.  
 PR 14-JUL-1998; 98WO-US014552.  
 PR 28-AUG-1998; 98WO-US017888.  
 PR 10-SEP-1998; 98WO-US018824.  
 PR 14-SEP-1998; 98WO-US019093.  
 PR 14-SEP-1998; 98WO-US019094.  
 PR 14-SEP-1998; 98WO-US019177.  
 PR 16-SEP-1998; 98WO-US019330.  
 PR 17-SEP-1998; 98WO-US019437.  
 PR 07-OCT-1998; 98WO-US021141.  
 PR 29-OCT-1998; 98WO-US022991.  
 PR 29-OCT-1998; 98WO-US022992.  
 PR 20-NOV-1998; 98WO-US024855.  
 PR 01-DEC-1998; 98WO-US025108.  
 PR 05-JAN-1999; 99WO-US000106.  
 PR 08-MAR-1999; 99WO-US005028.  
 PR 10-MAR-1999; 99WO-US005190.  
 PR 20-APR-1999; 99WO-US008615.  
 PR 14-MAY-1999; 99WO-US010733.  
 PR 02-JUN-1999; 99WO-US012252.  
 PR 01-SEP-1999; 99WO-US020111.  
 PR 08-SEP-1999; 99WO-US020594.  
 PR 13-SEP-1999; 99WO-US020944.  
 PR 15-SEP-1999; 99WO-US021090.  
 PR 15-SEP-1999; 99WO-US021547.  
 PR 05-OCT-1999; 99WO-US023089.  
 PR 29-NOV-1999; 99WO-US028214.  
 PR 30-NOV-1999; 99WO-US028313.  
 PR 30-NOV-1999; 99WO-US028409.  
 PR 01-DEC-1999; 99WO-US028301.  
 PR 01-DEC-1999; 99WO-US028634.  
 PR 02-DEC-1999; 99WO-US028551.  
 PR 02-DEC-1999; 99WO-US028564.  
 PR 16-DEC-1999; 99WO-US028565.  
 PR 16-DEC-1999; 99WO-US030095.  
 PR 20-DEC-1999; 99WO-US030911.  
 PR 20-DEC-1999; 99WO-US030999.  
 PR 22-DEC-1999; 99WO-US030720.  
 PR 30-DEC-1999; 99WO-US031243.  
 PR 05-JAN-2000; 2000WO-US000219.  
 PR 06-JAN-2000; 2000WO-US000277.  
 PR 11-FEB-2000; 2000WO-US000376.  
 PR 18-FEB-2000; 2000WO-US004341.  
 PR 22-FEB-2000; 2000WO-US004342.  
 PR 24-FEB-2000; 2000WO-US004914.  
 PR 24-FEB-2000; 2000WO-US005004.  
 PR 01-MAR-2000; 2000WO-US005601.  
 PR 02-MAR-2000; 2000WO-US005746.  
 PR 02-MAR-2000; 2000WO-US005841.  
 PR 10-MAR-2000; 2000WO-US006319.  
 PR 15-MAR-2000; 2000WO-US006884.  
 PR 20-MAR-2000; 2000WO-US007377.  
 PR 21-MAR-2000; 2000WO-US007532.  
 PR 30-MAR-2000; 2000WO-US008439.  
 PR 17-MAY-2000; 2000WO-US013705.  
 PR 22-MAY-2000; 2000WO-US014042.  
 PR 30-MAY-2000; 2000WO-US014941.  
 PR 02-JUN-2000; 2000WO-US015264.  
 PR 28-JUL-2000; 2000WO-US020710.  
 PR 11-AUG-2000; 2000WO-US022031.  
 PR 23-AUG-2000; 2000WO-US023522.  
 PR 24-AUG-2000; 2000WO-US023328.  
 PR 08-NOV-2000; 2000WO-US030952.  
 PR 10-NOV-2000; 2000WO-US030873.  
 PR 01-DEC-2000; 2000WO-US032678.  
 PR 20-DEC-2000; 2000WO-US034956.  
 PR 28-FEB-2001; 2001US-00796498.  
 PR 28-FEB-2001; 2001WO-US006520.  
 PR 01-MAR-2001; 2001WO-US006666.  
 PR 09-MAR-2001; 2001US-00802706.  
 PR 14-MAR-2001; 2001US-00808689.  
 PR 22-MAR-2001; 2001US-00816744.  
 PR 05-APR-2001; 2001US-00828366.  
 PR 10-MAY-2001; 2001US-00854208.  
 PR 10-MAY-2001; 2001US-00854280.  
 PR 18-MAY-2001; 2001US-00860216.  
 PR 25-MAY-2001; 2001US-00866028.  
 PR 25-MAY-2001; 2001US-00866034.  
 PR 25-MAY-2001; 2001WO-US017092.

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Job time : 156 secs

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XX
PA (GETH ) GENENTECH INC.
XX
PI Baker KP, Beresini M, Deforge L, Deanoyers L, Filvaroff E, Gao W;
PI Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;
PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;
XX
DR WPI; 2003-341980/32.
DR N-PSDB; ACD24025.
XX
XX
PT New secreted and transmembrane PRO nucleic acids, for treating
PT inflammation, organ failure, atherosclerosis, cardiac injury,
PT infertility, birth defects, premature aging, acquired immunodeficiency
PT syndrome (AIDS), or cancer.
XX
PS Claim 12; Fig 346; 660pp; English.
XX
CC The invention describes an isolated nucleic acid (I) comprising, or which
CC has 80 % sequence identity to, or the full-length coding sequence of, one
CC of 275 nucleotide sequences, and which encodes a corresponding
CC polypeptide selected from 275 amino acid sequences, where all sequences
CC are given in the specification. The polypeptide encoded by (I) is used to
CC detect PRO polypeptides, link a bioactive molecule to a cell expressing a
CC PRO polypeptide, modulate a biological activity of a cell, stimulate the
CC release of tumour necrosis factor (TNF)-alpha from human blood, modulate the
CC uptake of glucose or free fatty acid by cells, stimulate or inhibit
CC the proliferation or differentiation of cells or gene expression,
CC stimulate the release of proteoglycans, stimulate the release of cytokine
CC from peripheral blood mononuclear cells, inhibit the binding of A-peptide
CC to factor VIIa, or detect the presence of tumour in a mammal. The nucleic
CC acid and polypeptide encoded by it, are useful for treating inflammatory
CC diseases, organ failure, atherosclerosis, cardiac injury, infertility,
CC birth defects, premature aging, acquired immunodeficiency syndrome
CC (AIDS), cancer, or diabetic complications. The nucleic acid is useful as
CC hybridisation probes, in chromosome and gene mapping, and in generating
CC antisense RNA or DNA. The polypeptides are useful as pharmaceuticals,
CC diagnostics, biosensors or bioreactors. Both are useful in tissue typing.
CC This is the amino acid sequence of a novel human secreted and
CC transmembrane PRO polypeptide
XX
SQ Sequence 723 AA;
Query Match 57.0%; Score 527.5; DB 6; Length 723;
Best Local Similarity 64.8%; Pred. No. 1.6e-45;
Matches 114; Conservative 4; Mismatches 13; Indels 45; Gaps 4;
QY 1 TMNNLANCOREKDISVSIIGATGIXNTNKKADFXKGDSDKNGFQKARYPSVDYNLVQD 60
Db 589 TMNNLANCOREKDISVSIIGATGIXNTNKKADFXKGDSDKNGF-QARYPAVDYNLVQD 646
QY 61 LKGGDTAVRTSHSKRDTKCPQSGSGRRRG-PRPHSGXACCPCGSGGTGWSMNHCSV 119
Db 647 LKGGDTAVRDAHSKRDTKCPQSGSGEKGTPTLRG----- 683
QY 120 SLPKCSHAFIVDFLYFPFGSEASERKRPDSGCSTKDTKYQSVYVISEKDECVIA 175
Db 684 -----GEASERKRPDSGCSTKDTKYQSVYVISEKDECVIA 720
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